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(54) Title: cDNAs ENCODING MINOR AMPULLATE SPIDER SILK PROTEINS

(57) Abstract

cDNA clones encoding minor ampullate spidroin proteins (MiSP) are described. The translated amino acid sequence of the cloned cDNA shows that the MiSPs have a structure which exhibits an amino proximal nonrepetitive region, a repetitive portion and a carboxy-proximal nonrepetitive portion. The repetitive portion of the sequence is describable by a generic repeat formula. Comparison of the amino acid sequences derived from the translation with the sequences of short peptides obtained from solubilized minor ampullate spider silk suggests that the nonrepetitive portions of the protein are cleaved from the protein during secretion from the cells synthesizing the spidroins. This comparison also suggests that the minor ampullate spider silk is composed of at least three polypeptides.

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cDNAs Encoding Minor Ampullate Spider Silk Proteins

RELATED APPLICATIONS

The present application is related to copending application USSN 07/684,819, filed April 15, 1991, the entire contents of which are hereby incorporated by reference.

FIELD OF THE INVENTION

The present invention relates to polypeptides that form macroscopic fibers and to cloned DNA encoding such polypeptides.

The proteins are some of those which constitute silks made by spiders. Preferred embodiments of the present invention are those silk proteins made in the minor ampullate glands of the spider *Nephila clavipes*. The silks of the present invention also encompass fibers made from synthetic polypeptides of amino acid sequences derivable from the amino acid sequence of the *N. clavipes* ampullate silks or made from polypeptides expressed from cloned DNA obtained from a library of spider complementary or genomic DNA.

BACKGROUND OF THE INVENTION

The orb web spiders (*Nephila*) possess six types of silk synthetic glands, two of which are the major and minor ampullate organs. The major and minor ampullate

silks are distinguishable by their physical and chemical properties.

The major ampullate (dragline) silk possesses unique physical properties, combining high tensile strength and substantial elasticity [Denny, M.W. J. Exp. Biol., 65, 483-506 (1976); Lucas, F. Discovery, 25, 20-26 (1964)]. Previous investigations suggest that spider silk is composed of a single large protein, primarily containing pseudo-crystalline regions of stack ß-pleated sheet alternating with amorphous domains, [Warwicker, J.O., J.Mol.Biol., 2, 350-362 (1960); Lucase, F. et al, J.Text Inst., 46, T440-T452 (1985); Hepburn, H.R. et al., Insect Biochem., 9, 69-71 (1979)].

In fact, the major ampullate silk of *Nephila clavipes* was found to be composed of a composite of two proteins. cDNA clones encoding both of the proteins comprising the major ampullate silk are described in copending application USSN 07/684,819. We describe herein the isolation and characterization of cDNA clones encoding proteins composing minor ampullate silk.

SUMMARY OF THE INVENTION

Spider silk is composed of fibers formed from proteins. We have found that natural spider silk fibers are composites of two or more proteins. However, it is possible to form fibers from a single spider silk protein. In general, spider silk proteins are found to have primary amino acid sequences that can be characterized as indirect repeats of a short consensus sequence. Variation in the consensus sequence is then responsible for the distinguishable properties of the different silks proteins.

Furthermore, silk fibers can be made from synthetic polypeptides having amino acid sequences substantially similar to the consensus repeat unit of a silk protein or from polypeptides expressed from cloned DNA encoding a natural or engineered silk protein.

Thus, it is one object of the present invention to provide cloned DNA which encodes a spider silk protein. The cloned DNA is preferably obtained from an orb web spider (*Nephila*). Cloned cDNA from the minor ampullate gland of *Nephila clavipes* is described in detail below.

Naturally occurring spider silk proteins have an imperfectly repetitive structure. However, the imperfection in the repetition is likely to be a consequence of the process by which the silk protein genes evolved, rather than a requirement for fiber formation. The imperfection in repetition is thus likely to only subtly affect the characteristics of the fibers which form from the aggregation of the protein molecules. Accordingly, it is a second object of the present invention to provide cloned DNA encoding an engineered spider silk protein comprising a polypeptide having direct repeats of a unit amino acid sequence. Alternatively, the cDNA may include several different unit amino acid sequences to form a "copolymer" silk protein.

It is a third object of the invention to provide a spider silk protein expressed from a cloned DNA, wherein the cloned DNA is either one obtained from a spider ampullate gland cDNA, a genomic DNA, or synthetic DNA.

Finally, it is an additional object of the present invention to provide fibers made from silk protein obtained by expression of cloned DNA.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1A-1F shows the nucleotide and the amino acid sequence translation of the insert from pMISS1.

Figure 2A-2D shows the nucleotide and the amino acid sequence translation of the portions of the insert from pMISS2 that have been sequenced. 2A shows 309 nucleotides at the 5′ end of pMISS2. 2B shows 165 nucleotides of the PstI fragment 4 (see Figure 4). 2C, 2D show the 870 nucleotides at the 3′end of the insert

in pMISS2.

Figure 3A-3C shows the nucleotide and the amino acid sequence translation of the portions of the inserts from the 11-1 and 11-2 clones (pMISS3) that have been sequenced. 3A shows 165 nucleotides from the forward primer of the 11-1 clone. 3B shows 240 nucleotides from the reverse primer of the 11-1 clone. 3C shows 146 nucleotides from the forward primer of the 11-2 clone.

Figure 4 shows the alignment of the amino acid sequences of the nonrepetitive regions of MiSP1 and MiSP2.

Figure 5 shows a restriction map of the pMISS1 insert cDNA.

Figure 6 shows a restriction map of the pMISS2 insert cDNA. Beneath the restriction map is a schematic showing the portions of the insert that have been sequenced.

Figure 7 shows a flow chart description of the synthesis of the pET19b-16 vector. Restriction sites are designated as: B, Bsp E1; E, Eco RV; S, Sca I; X, Xma I.

Figure 8A-8B shows analysis of the purification of a synthetic spider silk protein expressed from the pET19b-16 vector. 8A shows analysis of the crude lysate at 1, 2 and 4 hours post-induction. 8B shows analysis of the protein purified by Ni^{2+} affinity purification.

DETAILED DESCRIPTION OF THE INVENTION

Studies in our laboratory have established that the major ampullate silk is composed of two distinct proteins. The major ampullate silk proteins possess the secondary structure predicted by Warwicker and others. The primary structure of the major ampullate silk proteins is characterized by indirect repeat of a discrete repeat unit. The sequence of the repeat unit is different for each of the proteins comprising the major ampullate silk.

The *Nephila* minor ampullate silk can be distinguished from the *Nephila* major ampullate silk by both physical and chemical properties. In contrast to the elasticity exhibited by the major ampullate silk, the minor ampullate silk is observed to yield without recoil. The minor silk will stretch about 25% of its initial length before breaking, exhibiting a tensile strength of nearly 100,000 psi. The amino acid composition of solubilized minor ampullate silk also differs from that of solubilized major ampullate silk.

Like the major ampullate silk proteins (major spidroin 1, MaSP1; major spidroin 2, MaSP2), the proteins comprising minor ampullate silk are found to have a primary structure dominated by imperfect repetition of a short sequence of amino acids. A "unit repeat" constitutes one such short sequence. Thus, the primary structure of the spider silk proteins is considered to consist mostly of a series of small variations of a unit repeat. The unit repeats in the naturally occurring proteins are often distinct from each other. That is, there is little or no exact duplication of the unit repeats along the length of the protein. However, synthetic spider silks can be made wherein the primary structure of the protein can be described as a number of exact repetitions of a single unit repeat. Additional synthetic spider silks can be described as a number of repetitions of one unit repeat together with a number of repetitions of a second unit repeat. Such a structure would be similar to a typical block copolymer. Of course, unit repeats of several different sequences can also be combined.

An alternative way to describe the primary structure of spider silk proteins is to consider a "consensus" sequence that is derived from an alignment of the unit repeats. Such a consensus sequence is the length of most of the unit repeats and accounts for the variation at each position of the unit repeat by

including the residue most common at each position. For the MaSP2 protein, the consensus sequence derived is GPGQQGPGGYGPGQQGPSGPGSAAAAAAAAAAGPGGY (see Table 2).

Cloned DNA of the present invention includes sequences shown in Figures 1A-1F, 2A-2C and 3A-3C. The cloned DNA of the present invention also includes DNA molecules made from *Nephila* DNA or RNA templates by PCR or the like, using primers made from sequences shown in Figures 1A-1F, 2A-2C and 3A-3C. Finally, cloned DNA of the present invention also encompasses polynucleotides which can hybridize to DNA having sequences shown in Figures 1A-1F, 2A-2C and 3A-3C under hybridization conditions typically used for library screening and Southern blotting. Preferably such hybridization conditions are those obtained by a solution of 6X SSC or SSPE, 5X Denhardt's solution, 0.5% SDS at a temperature of about 68°C, or those obtained by the same solution that is also 50% in formamide at a temperature of about 42°C. Alternatively, the hybridization conditions are those wherein the temperature is about 15-20°C below the T_m calculated for the solution conditions. [*See*, J. Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd ed., pp. 9.47 - 9.58, c. 1989 by Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY.].

The polypeptides of the present invention can be made by direct synthesis or by expression from cloned DNA. The means for expressing cloned DNA are generally known in the art. However, there are some considerations for design of expression vectors that are unusual for expressing DNA encoding the spider silk proteins of the present invention.

First, the proteins are highly repetitive in their structure. Accordingly, cloned DNA should be propagated and expressed in host cell strains that will maintain repetitive sequences in extrachromosomal elements (*e.g.* SURE™ cells, Stratagene). Also, due to the high content of alanine, glycine, proline, and glutamine, it might be

advantageous to use a host cell which overexpresses tRNA for these amino acids.

The proteins of the present invention can otherwise be expressed using vectors providing for high level transcription, fusion proteins allowing affinity purification through an epitope tag, and the like. The hosts can be either bacterial or eukaryotic. It is considered that yeast, especially *Saccharomyces cerevisisae*, or insect cells might be advantageous eukaryotic hosts.

Fibrillar aggregates will form by spontaneous self-assembly of spider silk proteins when the protein concentration exceeds a critical value. The aggregates can be gathered and mechanically spun into macroscopic fibers according to the method of O'Brien et al. [I. O'Brien et al., "Design, Synthesis and Fabrication of Novel Self-Assembling Fibrillar Proteins", in Silk Polymers: Materials Science and Biotechnology, pp. 104 - 117, Kaplan, Adams, Farmer and Viney, eds., c. 1994 by American Chemical Society, Washington, D.C.].

The following examples are provided to illustrate the invention in more detail. The examples are not to be taken as limiting the invention, the scope of which is rather defined by the claims following.

Example I: cDNA Clones Encoding Minor Ampullate Silk Proteins

The minor ampullate glands are small, J-shaped organs located in the abdomen of the spider. The minor ampullate glands (about 20) were removed from a number of spiders and frozen in liquid nitrogen. Total RNA was prepared from the frozen tissue by standard methods. cDNA was prepared from the total RNA using the RIBOCLONE™ system (Promega). The synthesis method was modified slightly by using pseudorandom hexamers in addition to the NotI primer-adapter in the primer extension steps. The pseudorandom hexamers were

synthesized having the sequence (A or T)(G or C)(G or C)(A or T)(G or C)(G or C). Such hexamers reflect the sequence bias in the minor ampullate silk proteins (minor spidroins, MiSP) we hypothesized would be imposed by repetition of alanine and glycine residues, which are found in large proportion in the amino acid composition of solubilized minor ampullate silk. We anticipated that so biasing the primer composition would enrich the library in long cDNAs encoding MiSP proteins.

The cDNA thus synthesized was ligated to appropriately digested pGEM3Zf(-) plasmid (Promega) and the ligation mixture was used to transform SURE™ *E. coli* cells (Stratagene). Plasmid DNA was prepared from randomly selected transformed colonies and the insert DNA was partially sequenced, using the forward and reverse primers provided by the supplier (Promega), that are complementary to the vector sequence near the insert. Clones having inserts encoding highly repetitive sequences were examined in greater detail with respect to insert size. Clones having an insert size greater than 1.5 kbp were sequenced in their entirety.

The entire insert of the pMISS1 (encoding MiSP1) has been sequenced. The nucleotide sequence and the resulting translation are shown in Figure 1. A restriction map is shown as Figure 5. The region from nucleotides 96-137 is represented as indeterminate. That portion of the cDNA is found to have a much higher GC content than the remainder of the sequence. As a result, that portion of the nucleotide sequence has not been resolved due to "compression" observed in the electrophoresis step. pMISS1 contains an open reading frame beginning with the ATG start codon at nucleotides 183-185. The open reading frame encodes a 5'-nonrepetitive region, an indirect repetitive region and a 3'-nonrepetitive region. The 5'-nonrepetitive region contains a sequence of about 16 residues (amino acids

2-17) that conforms to secretion signal sequences. The presence of the leader peptide suggests that the MiSP1 protein is processed and secreted through the endoplasmic reticulum.

Table 1 shows the MiSP1 amino acid sequence formatted to show the 13 unit repeats of the MiSP1 protein.

Table 1

Minor Ampullate Spidroin 1 Residues 92-706, showing alignment of unit repeats:

```
  GAAGAGGYGRGAG----------------GYGGQGGYGAGAGAGAAAAA
GAGAGGAGGYGRGAGAGAGAAAGAGAGAGGAGYGGQGGYGAGAGAGAAAAA
GAGAGGAGGYGRGAGAGAGAAAGAGA----GGYGGQGGYGAGAGAGAAAAAA
GAGSGGAGGYGRGAGAGAGAAAGAGAGA--GSYGGQGGYGAGAGAGAAAAA
GAGAGGAGGYGRGAGAGAGAGAGAAARAGAGAGG------------AAAAA
GAGAGGAGGYGRGAGAGAGAAAGAGAGA------GGYGGQSGYGAGAG--AAAAA
GAGAGGAGGYGRGAGAGAGAAAGAGAGAAAGAGAGGYGGQGGYGAGAGAGAAAAA
GAGAGGAGGYGRGAGAGAGAAAGAGAG----GYGGQGGYGAGAGAGAAAAA
-TGAGGAGGYGRGAGAGAGAAAGAGAGTGGAGYGGQGGYGAGAGAGAAAAA
GAGAGGAG-YGRGAGAGAGAAAGAGAGAAAGAGAGAGGYGGQGGYGAGARAGAAAAA
GAGAGGAAGYSRGGRAGAAGAGAGAAAGAGAGAGGYGGQGGYGAGAGAGAAAAA
GAGSGGAGGYGRGAGAGAAAGAGAAAGAGAGAGGYGGQGGYGAGAGAAAAA
GAGAGRGGYGRGAGAGGYGGQGGYGAGAGAGAAAAA
```

- added for purposes of alignment

Each repeat is a variation of the consensus amino acid sequence RGAAGAAGAGAGAAAGAGAGAGAGGYGGQGGYGAGAGAGAAAAAGAGAGGAGGYG. This repetitive region can be described as a mixture of two types of units, (1) dimers of alanine separated by glycine residues, and (2) dimers of glycine separated by tyrosine or glutamine residues. It is thus distinguishable from the consensus sequence of the MaSP2 protein, which can be characterized as predominantly dimers of glycine or glutamine separated by proline or tyrosine residues.

Alternatively, the majority of the amino acid sequence of the MiSP1 protein can be described by a repeat unit having the generic formula:

$$(GR)(GA)_l(A)_m(GGX)_n(GA)_l(A)_m$$

where X is tyrosine, glutamine or alanine and where l = 1 to 6, m = 0 to 4 and n = 1 to 4. This finding is similar to what was observed for the MaSP1 and MaSP2 proteins, which exhibit the generic formulas:

MaSP1:

$$(XGG)_w(XGA)(GXG)_x(AGA)y(G)_zAG$$

where X is tyrosine or glutamine and where w = 2-3, x = 1-3, y = 5-7, and z = 1 or 2.

MaSP2:

$$(GPG_2YGPGQ_2)_a(X)_2S(A)_b$$

where X = GPG or GPS and where a = 2 or 3 and b = 7 to 10.

Inspection of the amino acid sequence of MiSP1 shows that, for the most part, the protein can be viewed as a derivatized polyamide. Accordingly, polypeptide having the less complex generic formula:

$$(GGX)_n(GA)_m(A)_l$$

where X is tyrosine, glutamine or alanine and where l = 1 to 6, m = 0 to 4 and n = 1 to 4,

would also be expected to have many of the properties of the MiSP1 protein.

The 3'-nonrepetitive coding region of pMISS1 encodes a 96 amino acid spider silk consensus sequence that is 50% and 49% identical to the 3'-nonrepetitive regions of MaSP1 and MaSP2, respectively. The coding region ends at nucleotide position 2634 with a TAA stop codon. The 3' untranslated region of pMISS1 contains a poly(A) tail.

The majority of the pMISS2 (encoding MiSP2) cDNA has been sequenced. The insert in pMISS2 is 1.6 kbp in length, of which 1344 nucleotides have been determined. The nucleotide sequence and translation of the completed portions of the DNA sequence are shown in Figure 2. Figure 6 shows a restriction map of the pMISS2 clone and indicates what portions of the cDNA insert have been sequenced. pMISS2 contains an open reading frame beginning at the 5' end of the insert that does not begin with a methionine. This result strongly suggests that the pMISS2 cDNA lacks nucleotides encoding the amino terminus of the MiSP2 protein. The pMISS2 cDNA, like the pMISS1 cDNA encodes a 5'-nonrepetitive region, a repetitive region and a 3'-nonrepetitive region. The 5'- and 3'- nonrepetitive regions of MiSP1 and MiSP2 are aligned in Figure 4. In contrast to MiSP1, the unit repeat that characterizes the repetitive region in MiSP2 is cryptic. As no clear unit repeat is yet distinguishable, no consensus repeat unit is yet derived. However, it is clear from inspection of the repetitive portion of MiSP2 that it is distinguishable from the repetitive portion of MiSP1.

Another pair of clones, designated 11-1 and 11-2, respectively (collectively pMISS3), are independent

isolates of the same cDNA and are found to encode a third minor ampullate silk polypeptide (MiSP3). 11-1 contains a 2 kbp insert; 11-2 contains a 1.5 kbp insert. Partial nucleotide sequences have been obtained from both of these clones to date. The nucleotide sequences and translations thereof are presented as Figures 3A-3C.

Three different types of N-bromosuccinimide (NBS) peptides from minor ampullate silk have been purified. The first type of peptide has the amino acid sequence GGQGGY. The second type of peptides have a sequence encompassed by the generic formula $(GA)_n$, where n=3.5, 4.5, or 8.5. The third type of peptides have the sequence $(G)_n$, where n=6 or 9. The pMISS1, pMISS2, and pMISS3 clones all encode the GGQGGY peptide and some variation of the $(GA)_n$ peptide. However, none of the isolated cDNAs, so far as they have been characterized to date, encode a $(G)_n$ peptide. Since pMISS1 has been completely sequenced, except for a small region of 42 nucleotides in a highly compressed region (high GC content) and does not contain the $(G)_n$ peptide, the minor ampullate silk must contain at least two proteins. Furthermore, while portions of the nonrepetitive regions of MiSP2 are identical to parts of the nonrepetitive regions MiSP1, the nonrepetitive regions of the two proteins are different. Also, the repetitive regions are different of MiSP1 and MiSP2 are distinguishable (see below). Although nonrepetitive portions have not yet been found in MiSP3, the repeats encoded by the 11-series isolates are distinguishable from the repeats of both MiSP1 and MiSP2 on two bases: (1) the spacing between Gln residues is only about one-half that seen in MiSP1 and MiSP2, and (2) Phe residues occasionally precede the GGQGGY sequence whereas a Tyr always precedes the GGQGGY sequence in MiSP1. Thus, the minor ampullate gland produces a silk comprised of at least three proteins.

Example 2: Expression of a cDNA Encoding a Polypeptide Comprising the MaSP2 consensus sequence

In order to demonstrate expression of an engineered spider silk protein, the consensus sequence from the MaSP2 protein (USSN 07/684,819 was cloned into an *E. coli* expression vector. The consensus sequence was determined, using the considerations described above, from the alignment of the unit repeats of the MaSP2 protein. Table 2 shows the alignment of the unit repeats of the MaSP2 protein.

Table 2

Alignment of Unit Repeats of the MaSP2 Protein

```
GPGQQGPGGYGPGQQGP--SGPGSAAAAAAAAA-----GPGGYGPGQQGPGGY
GPGQQGPGRYGPGQQGP--SGPGSAAAAAA-------------GSGQQGPGGY
GPRQQGPGGYGQGQQGP--SGPGSAAAASAAASAESGQQGPGGYGPGQQGPGGY
GPGQQGPGGYGPGQQGP--SGPGSAAAAAAAS------------GPGQQGPGGY
GPGQQGPGGYGPGQQGP--SGPGSAAAAAAAAS-----------GPGQQGPGGY
GPGQQGPGGYGPGQQGL--SGPGSAAAAAAA----------------------
GPGQQGPGGYGPGQQGP--SGPGSAAAAAAAAA----------------GPGGY
GPGQQGPGGYGPGQQGP--SGAGSAAAAAAA------------GPGQQGLGGY
GPGQQGPGGYGPGQQGPGGYGPGSASAAAAAA----------------------
GPGQQGPGGYGPGQQGP--SGPGSASAAAAAAAA---------------GPGGY
GPGQQGPGGYAPGQQGP--SGPGSASAAAAAAAA---------------GPGGY
GPGQQGPGGYAPGQQGP--SGPGSAAAAAAASA----------------GPGGY
```

The synthesis of the expression vector is described below and shown schematically in Figure 7.

Two synthetic oligonucleotides were synthesized:

1) an 84 base oligonucleotide, named S2long

5'-TCTAGCCCGGGTGGCTATGGTCCTGGACAGCAAGGTCCTGGCGGTTACGGTCC
TGGCCAACAGGGTCCCTCTGGTCCAGGCAGT-3'

2) a 59 base oligonucleotide, named S2short

5'-TCCGGACCTGCTGCGGCGGCTGCGGCAGCTGCACTGCC
TGGACCAGAGGGACCCTGTTG- 3'

These oligonucleotides were designed to hybridize to each other in a 27 base region of complementarity, on the 3' end of each respective oligonucleotide. When the rest of the bases were filled in by VENT™ polymerase (New England Biolabs) and the product digested with Xma I (recognition site-CCCGGG), a double-stranded segment of DNA resulted which encoded the basic repetitive unit of MaSP2 (in single letter amino acid code):

PGGYGPGQQGPGGYGPGQQGPSGPGSAAAAAAAAG

The DNA segment, with an Xma I cut on the 5' end (with respect to the coding strand) and the other end blunt but containing a Bsp EI site, was ligated into pBLUESCRIPT™ II (Stratagene) which had been double digested with Xma I and Eco RV and agarose gel purified, thus giving a directional cloning with the inserted segment in frame with the lac I gene of pBLUESCRIPT™ II. It is important to note for the strategy explained later that Xma I and Bsp E I have compatible, nonregenerable overlaps. That is, DNA cut with these enzymes can be ligated, but the ligation will not regenerate either site. The ligated DNA was subjected to Eco RI digestion to reduce background (the Xma I, Eco RV digest of the vector eliminated the unique Eco RI site of pBLUESCRIPT™

II) and used to transform competent SURE™ *E. coli* cells (Stratagene).

Twelve white colonies (indicating inserts were present in the plasmid) resulted which were screened by digesting plasmid DNA obtained from the colonies (SCREENMAX™, J.T. Baker) with BssHII to release the insert. The insert sizes were determined by agarose gel electrophoresis.

Four colonies contained inserts of the predicted size. Plasmid DNA was prepared from those colonies by SCREENMAX™ and subjected to sequencing. One colony harbored a plasmid (hereafter referred to as pS2U) containing an insert that was usable, although its structure was not exactly as designed. The ninth base of S2short was changed to a G, most likely a result of a synthesis error, although the difference may also have been a mistake incorporated by the polymerase or a mutation occurring during the cloning manipulations. In addition, the first base of S2short is missing (or the first base of the Eco RV site, it is impossible to determine which). This could be due to nonspecific nuclease activity in restriction enzymes used to perform the recombinant DNA manipulations. However, these changes are not critical, since the G appears in a wobble position in the coding sequence, and the alteration of the blunt end ligation site may even have provided some advantages, putting several codons for arginine directly after the MiSP2 sequence.

The insert was doubled, except for the additional arginine encoding codons, by manipulation of the restriction sites imbedded by design at the ends of the unit consensus sequence as well as a unique Sca I site in the ampicillin resistance gene of pBLUESCRIPT™ II (See Figure 7). Plasmid from a miniprep is digested with Sca I, then divided into two aliquots. One aliquot is digested with Xma I and the other with Bsp E I. The digests are electrophoresed on 0.8% soft agarose, and

the appropriate bands excised with a razor blade, and the DNA extracted using the standard procedure provided with β-agarase (New England Biolabs). The Sca I-Xma I segment containing one copy of the unit is then ligated to the Sca I-Bsp EI segment also containing one copy of the unit, thus effectively doubling the insert size while keeping both units in frame and regenerating the ampicillin resistance. This strategy can be repeated to derive any number of repeats of the unit desired (until secondary structure or insert size interferes). Thus an engineered vector encoding a polypeptide comprising 16 repeats of the MaSP2 consensus sequence was constructed in pBLUESCRIPT™ II.

The insert encoding 16 repeating units of the MaSP2 consensus sequence was placed in pET19b by cutting the HincII site of pBLUESCRIPT™ (creating a blunt end) then ligating a Bam H1 linker of the appropriate size to that end. The fragment was then subjected to Bam H1 cleavage, which cut at both ends, due to the presence of a Bam H1 site in pBLUESCRIPT™ a few bases 5′ of the insert. This 5′ Bam H1 site was engineered to be in frame with the Bam H1 insertion site of the pET system of vectors (Novagen). As noted below, the pET vector system allows affinity purification of expressed proteins using affinity recognition of a polyhistidine leader sequence attached to the desired protein. The insert was agarose gel purified, ligated into Bam H1-cut, phosphatased pET19b and the result used to transform competent SURE™ *E. coli* (Stratagene). The resultant colonies were screened and the orientation of the inserts determined by restriction digest. Clones with properly oriented inserts were then used for expression experiments.

BL31 DE3 *E. coli* (Novagen) were transformed with a plasmid having the insert in the desired orientation (pET19b-16) and plated on LB agarose plates containing chloramphenicol and carbenicillin. Antibiotic resistant colonies were picked an grown in LB medium containing

chloramphenicol and carbenicillin to an OD_{600} of about 0.8. One mL of the resulting inoculum was saved as a freezer stock. Inoculum cultures should be grown to OD_{600} of 0.8 or less, in order to maintain antibiotic selection pressure.

Five mL of the inoculum was used to inoculate 50 mL of LB containing the antibiotics. When the OD_{600} reached 0.8, the cells were collected by centrifugation and resuspended in 50 mL of fresh medium. The resuspended culture was diluted into 500 mL of LB containing the antibiotices and culture was continued until the OD_{600} reached 0.8. IPTG was added to a concentration of 0.8 mM to initiate expression of the synthetic spider silk gene.

After four hours, the cells were collected by centrifugation and resuspended in a lysis buffer modified from the method of Sambrook et al. (50 mM Tris-Cl (pH 8.0), 10 mM $MgCl_2$, 100 mM NaCl), and lysed with lysozyme in the presence of PMSF according to Sambrook et al. [J. Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd ed., pp. 17.23-17.44, c. 1989 by Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY.].

The MaSP2 consensus polypeptide was purified from the lysate by affinity purification using a Ni^{2+} column, as described by the technical manual provided by the manufacturer (Novagen). The divalent metal complexes the polyhistidine leader sequence encoded by the pET vector. A single step affinity purification provided the desired fusion protein at 95% purity.

For cleavage of the polyhistidine leader peptide, the eluant from the affinity column was dialysed against distilled water for 24 hours to remove salts. The solution was made to 25 mM in ammonium bicarbonate and TPCK-treated trypsin was added to 1/20 the amount of the protein content of the eluate by weight. The digestion reaction was incubated at 37°C for 4 hours. An

additional aliquot of trypsin was added and the incubation was continued for an additional 4 hours. The leader peptide fragment was separated from the synthetic spider silk polypeptide by gel filtration chromatography on SEPHADEX™ G-50. Figure 8 shows the results obtained using the above-described system. Approximately 10 mg of the MiSP2 consensus polypeptide are obtained from a 500 mL culture. The molecular weight of 58 kDa is the expected molecular weight for the polypeptide having a sequence of 16 repeats of the MiSP2 consensus sequence.

Example 3: A Generalized Method for Preparing Vectors for Expression of Spider Silk Protein Consensus Polypeptides

Following is a general method for generating artificial genes for any repetitive protein that contains polyalanine stretches. The method can thus be applied to express a protein comprising the consensus polypeptide of any of the major or minor ampullate spidroin proteins described herein.

The method employs two particular restriction enzymes, Sfi I and AlwN I (recognition sites shown below):

Sfi I : GGCCNNNN/NGGCC AlwN I : CAGNNN/CTG

An oligomer is designed such that a Bam HI site is in frame with and immediately precedes an Sfi I site. The Bam H I site will also be in frame with the pET system of vectors which are used for expression. However, the manipulations which are needed to produce multiple copies of the artificial unit will not involve this site, since it is 5′ to the Sfi I site. Sfi I and AlwN I are used as the primary enzymes for manipulations for unit multiplication because the recognition sequences of both of these enzymes can (1) code for polyalanine stretches (see below) and (2) can form a pair of compatible, nonregenerable sites.

Ala Ala Ala Ala Ala Ala Ala

Sfi I : G/GCC/GCA/GCG/GCC AlwN I : GCA/GCA/GCT

Two oligonucleotides are designed that will reverse complement each other on their 3′ ends, allowing hybridization. The first contains the Bam HI site, followed (in frame) by the Sfi I site representing the polyalanine region of MiSP1, followed by DNA encoding approximately two-thirds of the repetitive portion of MiSP1. The second oligonucleotide will be the anti-coding strand of MiSP1, starting with an AlwN I site and encoding approximately two-thirds of the repetitive region.

The simple diagram below shows the intended overlap of the the oligonucleotides and the placement of the restriction enzymes sites.

5′ B-S----------
----------A 5′

After hybridization, the overhanging ends are filled with VENT™ polymerase. The resultant double-stranded product is digested with Bam H I and, after agarose gel purification, cloned into a Bam H I cut, Eco R V cut pBLUESCRIPT™ II vector. This ligation mixture is digested with Eco R I (to reduce background) and used to transform competent SURE™ *E. coli* cells. Plasmid DNA is prepared from resulting colonies and screened first for insert size, then sequenced to determine if the insert is properly integrated.

To double the insert to appropriate size, double digests with Sca I (found in the Amp′ gene of BLUESCRIPT™) and either Sfi I or AlwN I are performed and the resultant fragments gel purified. The 5′ Sca I-Sfi I-AlwN I 3′ fragment of the Sca I + AlwN I digest is ligated to the 5′ Sfi I-AlwN I-Sca I 3′ fragment from the Sca I + Sfi I digest. This will regenerate a

functional pBLUESCRIPT™ II which will include a doubled artificial gene. Since Sfi I and AlwN I ends are compatible they will ligate, but the resulting splice site will not regenerate a recognition site for either enzyme. This allows the doubling to be extended to 4-, 8-, 16-, and higher multimers of the original insert.

The final vector+multimer can then be cut with Hinc II, ligated with Bam H I linkers of an appropriate length, cut with Bam H I to liberate the insert, and cloned directly into the pET system of vectors for expression.

Example 4: Optimization of Expression of DNA Encoding Spider Silk Proteins

In order to increase the yield of spider silk proteins expressed from cloned DNA in bacteria, the above-described culture methods can be modified. In particular, due to the large proportion of glycine, alanine, glutamine and proline in the proteins, supplementation of the culture medium used to grow cells for expression with these amino acids is expected to allow increased yield of the spider silk protein. Also, the culture density can be increased by use of high-density fermentation methods standard in the art [*See, e.g.* Reisenburg et al., Applied Microbiology and Biotechnology 34:77 (1990); Alberghina et al., Applied Microbiology and Biotechnology 34:82 (1990)]. For instance, increasing the OD_{600} at which expression is initiated from 0.8 to 20 would be expected to produce a concomittant increase in yield from 20 mg/L to 480 mg/L.

The vector used to support replication of the cloned DNA and to drive its expression can also be changed. The basic pET system described above is available from the supplier (Novagen) in many variations. One characteristic which makes the pET system advantageous is that expression of inserts in the pET vectors is very tightly regulated. Very little of the cloned DNA is

expressed until transcription of the insert DNA is induced. When transcription is induced, additional elements of the pET vector inhibit production of host cell proteins, thereby putting most of the protein synthetic resources of the cell to work to make protein encoded by the insert DNA.

However, the use of chloramphenicol and carbenicillin resistance to provide selection pressure is disadvantageous for high-level expression of proteins. Accordingly, use of a different antibiotic selection, *e.g.* kanamycin resistance, is expected to provide increased yields of protein by expression of DNA cloned in pET vectors.

Another advantage of the system used in the present case is that the polyhistidine leader peptide provides an affinity purification method that can be used even in the presence of chaotropic agents. This would allow purification of spider silk proteins fused to such a polyhistidine sequence which might be made in "inclusion bodies", aggregates of insoluble protein, that require harsh solubilization procedures prior to purification.

The host cell strain used for expression can also be optimized. Cells having a high level of tRNA for Ala, Gln, Gly and Pro codons could be made and used for expression of spider silk proteins. Also, the cellular protease complement of the cells can be manipulated to minimize degradation of the expressed protein.

It is considered that the spider silk proteins of the present invention can be expressed in appropriately engineered insect cells, using commonly available baculovirus vectors.

Example 5: Preparation of Fibers From Spider Silk Proteins

As noted above, the spider silk proteins can be viewed as derivatized polyamides. Accordingly, the methods for producing fiber from soluble spider silk

proteins is similar to that used to produce typical polyamide fibers, *e.g.* nylons, and the like.

O'Brien et al. [*supra*] describe fiber production from adenovirus fiber proteins. In a typical fiber production, the spider silk proteins are solubilized in a strongly polar solvent. The protein solution is typically greater than 5% in protein concentration. The solution is preferably between 8 and 20% in protein.

Fibers are preferably spun from solutions demonstrating properties indicating a liquid crystal phase. The concentration at which the phase transition will occur is different for particular polypeptide compositions. However, the phase transition can be monitored by observing the clarity and birefrigence of the solution. Onset of the a liquid crystal phase is detected by a translucent appearance of the solution and the observation of birefringence when the solution is viewed through crossed polarizing filters.

The solvent used to dissolve the spider silk protein is preferably highly polar. Such solvents are exemplified by di- and tri- haloacetic acids, haloalcohols (*e.g.* hexafluoroisopropanol). In some instances, co-solvents such as acetone are useful. Also, solutions of chaotropic agents, such as lithium thiocyanate, guanadine thiocyanate or urea can be used.

In one fiber-forming technique, fibers are first extruded from the protein solution through an orifice into methanol, until a length sufficient to be picked up by a mechanical means is produced. Then the fiber is pulled by such mechanical means through the methanol solution, collected and dried. The methods for drawing fibers are considered well-known in the art. Fibers made from the 58 kDa synthetic MaSP consensus polypeptide, described in Example 2, for instance, can be drawn by methods similar to those used for drawing low molecular weight nylons.

The invention being thus described, various

modifications of the materials and methods disclosed herein will be apparent to one of skill in the art. Such modifications are to be considered encompassed by the scope of the invention described by the claims below. Articles of the scientific and patent literature cited herein are incorporated by reference in their entirety by such citation.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Lewis, Randolph V.
Colgin, Mark

(ii) TITLE OF INVENTION: cDNAs Encoding Minor Ampullate Spider Silk Proteins

(iii) NUMBER OF SEQUENCES: 56

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Birch, Stewart, Kolasch & Birch
(B) STREET: P.O. Box 747
(C) CITY: Falls Church
(D) STATE: Virginia
(E) COUNTRY: USA
(F) ZIP: 22040-3487

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/209,747
(B) FILING DATE: 14-MAR-1994
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Murphy Jr., Gerald M.
(B) REGISTRATION NUMBER: 28,977
(C) REFERENCE/DOCKET NUMBER: 1447-104P

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 703-205-8000
(B) TELEFAX: 703-205-8050

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2793 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Nephila clavipes
(F) TISSUE TYPE: minor ampullate gland

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 183..2675
(D) OTHER INFORMATION: /product= "N. clavipes minor ampullate silk protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ACATACTAGG TTTGGTGCCG GAGCTGGAGC TGGTACGTCT GTGCAGAAAT ACTTTGCACA 60

TCACTTCTCC AATTGCTTCT CGGGTATTTG TCAAATGATT AGTTCTACAA CTTCTACTGA 120

TCATGCAGTA AGTGTTGCTA CGAGCGTTGC GCTGAAGTCA GCTTGGACTT GATGCAAATG 180

CTATGAACAA CTTACTAGGT GCCGTTAGTG GATATGTTTC GACACTAGGC AACGCTATTT 240

CTGATGCTTC GGCATACGCA AATGCTCTTT CTTCCGCTAT AGGAAATGTG TTAGCTAATT 300

CCGGTTCAAT TAGCGAAAGC ACTGCATCTT CTGCTGCTTC CAGTGCTGCT TCTTCAGTCA 360

CTACAACTTT GACGTCTTAT GGACCAGCTG TATTTTACGC ACCTTCTGCA TCATCTGGAG 420

GCTATGGAGC TGGAGCTGGA GCTGTTGCTG CAGCAGGAGC TGCCGGCGCT GGAGGTTACG 480

GAAGAGGTGC TGGAGGCTAC GGTGGACAAG GAGGATATGG TGCCGGAGCC GGAGCTGGTG 540

CTGCTGCAGC TGCTGGAGCA GGAGCCGGAG GCGCTGGTGG TTACGGTAGA GGTGCTGGTG 600

CTGGAGCTGG TGCGGCTGCT GGGGCAGGTG CAGGCGCCGG TGGTGCTGGA TATGGTGGAC 660

AAGGCGGATA TGGTGCCGGA GCAGGAGCTG GTGCGGCTGC TGCTGCTGGT GCAGGAGCAG 720

GAGGTGCTGG CGGTTACGGT AGAGGTGCTG GTGCTGGAGC AGGAGCCGCT GCGGGTGCTG 780

GAGCTGGAGG CTACGGTGGT CAAGGTGGGT ACGGTGCCGG AGCAGGAGCT GGTGCGGCTG 840

CTGCTGCTGC TGGAGCAGGA TCTGGAGGCG CTGGCGGTTA CGGTAGAGGT GCTGGTGCTG 900

GAGCTGGAGC CGCTGCAGGT GCAGGAGCAG GAGCTGGAAG CTACGGTGGT CAAGGATACG 960

GTGCCGGAGC AGGAGCTGGT GCTGCTGCAG CTGCANNNNN NNNNNNNNNN NNNNNNNNNN 1020

NNNNNNNNNN NNNNNNNGGT GCAGGTGCAG GTGCTGGATA TGGTGGACAA GGCGGATATG 1080

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GTTACGGTAG AGGTGCTGGT GCTGGAGCTG GAGCCGCTGC AGGTGCAGGA GCAGGAGCTG 1200

GAGGCTACGG TGGTCAAAGT GGATACGGTG CCGGAGCAGG AGCTGCTGCA GCTGCTGGAG 1260

CAGGAGCTGG AGGCGCTGGT GGTTACGGTG AGGTGCTGGT GCTGGAGCAG GAGCCGCTGC 1320

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GTACGGTGCC GGTGCAGGAG CTGGTGCGGC TGCTGCTGCT GGAGCAGGAG CTGGAGGCGC 1440

TGGTGGTTAC GGTAGAGGTG CTGGTGCTGG AGCTGGAGCT GCTGCAGGCG CAGGAGCTGG 1500

AGGCTACGGT GGTCAAGGTG GATACGGTGC CGGAGCAGGA GCTGGTGCTG CTGCAGCTGC 1560

TGCAACAGGA GCCGGAGGCG CTGGTGGTTA CGGTAGAGGT GCTGGTGCTG GAGCTGGTGC 1620

CGCTGCTGGG GCAGGTGCAG GCACCGGTGG TGCTGGATAT GGTGGACAAG GCGGTTATGG 1680

TGCCGGAGCA GGAGCTGGTG CGGCTGCTGC TGCTGGTGCA GGAGCAGGAG GTGCTGGTTA 1740

CGGTAGAGGT GCTGGTGCTG GAGCTGGAGC TGCTGCAGGT GCTGGAGCTG GAGCCGCTGC 1800

AGGTGCAGGA GCAGGAGCTG GAGGCTACGG TGGTCAGGGT GGATACGGTG CCGGAGCAAG 1860

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TGGAGCCGGT GCTGCTGCAG CTGCTGGAGC GGGAGCCGGA GGCTATGGCG ACAAGGAGAT 2340

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CGAAGCATCT TCTAGGATAT CGTCGGCGGC TTCCACTTTA GTATCTGGAG GTTACTTGAA 2460

TACAGCAGCT CTGCCATCGG TTATTTCGGA TCTTTTTGCC CAAGTTGGTG CATCTTCTCC 2520

GGTGATCAGA CAGCGAAGTT TGATCCAAGT TTTGTTGGAA ATTGTTTCTT CTCTTATCCA 2580

TATTCTCAGT TCTTCTAGCG TAGGACAAGT CGATTTCAGT TCGGTTGGGT CGTCTGCTGC 2640

AGCTGTTGGT CAATCCATGC AAGTTGTAAT GGGCTAAACA TGATGGTTCT CTCAATTATG 2700

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AAAATTCTTT TCTGCAAAAA AAAAAAAAAA AAA 2793

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 832 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:
(A) ORGANISM: N. clavipes
(F) TISSUE TYPE: minor ampullate gland

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asn Asn Leu Leu Gly Ala Val Ser Gly Tyr Val Ser Thr Leu Gly
1 5 10 15

Asn Ala Ile Ser Asp Ala Ser Ala Tyr Ala Asn Ala Leu Ser Ser Ala
20 25 30

Ile Gly Asn Val Leu Ala Asn Ser Gly Ser Ile Ser Glu Ser Thr Ala
35 40 45

Ser Ser Ala Ala Ser Ser Ala Ala Ser Ser Val Thr Thr Thr Leu Thr
50 55 60

Ser Tyr Gly Pro Ala Val Phe Tyr Ala Pro Ser Ala Ser Ser Gly Gly
65 70 75 80

Tyr Gly Ala Gly Ala Gly Ala Val Ala Ala Ala Gly Ala Ala Gly Ala

85 90 95

Gly Gly Tyr Gly Arg Gly Ala Gly Gly Tyr Gly Gly Gln Gly Gly Tyr
100 105 110

Gly Ala Gly Ala Gly Ala Gly Ala Ala Ala Ala Ala Gly Ala Gly Ala
115 120 125

Gly Gly Ala Gly Gly Tyr Gly Arg Gly Ala Gly Ala Gly Ala Gly Ala
130 135 140

Ala Ala Gly Ala Gly Ala Gly Ala Gly Gly Ala Gly Tyr Gly Gly Gln
145 150 155 160

Gly Gly Tyr Gly Ala Gly Ala Gly Ala Gly Ala Ala Ala Ala Ala Gly
165 170 175

Ala Gly Ala Gly Gly Ala Gly Gly Tyr Gly Arg Gly Ala Gly Ala Gly
180 185 190

Ala Gly Ala Ala Ala Gly Ala Gly Ala Gly Gly Tyr Gly Gly Gln Gly
195 200 205

Gly Tyr Gly Ala Gly Ala Gly Ala Gly Ala Ala Ala Ala Ala Ala Gly
210 215 220

Ala Gly Ser Gly Gly Ala Gly Gly Tyr Gly Arg Gly Ala Gly Ala Gly
225 230 235 240

Ala Gly Ala Ala Ala Gly Ala Gly Ala Gly Ala Gly Ser Tyr Gly Gly
245 250 255

Gln Gly Tyr Gly Ala Gly Ala Gly Ala Gly Ala Ala Ala Ala Ala Xaa
260 265 270

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Ala
275 280 285

Gly Ala Gly Ala Gly Tyr Gly Gly Gln Gly Gly Tyr Gly Ala Gly Ala
290 295 300

Gly Ala Gly Ala Ala Ala Ala Ala Gly Ala Gly Ala Gly Gly Ala Gly
305 310 315 320

Gly Tyr Gly Arg Gly Ala Gly Ala Gly Ala Gly Ala Ala Ala Gly Ala
325 330 335

Gly Ala Gly Ala Gly Gly Tyr Gly Gly Gln Ser Gly Tyr Gly Ala Gly
340 345 350

Ala Gly Ala Ala Ala Ala Ala Gly Ala Gly Ala Gly Gly Ala Gly Gly
355 360 365

Tyr Gly Arg Gly Ala Gly Ala Gly Ala Gly Ala Ala Ala Gly Ala Gly
370 375 380

Ala Gly Ala Ala Ala Gly Ala Gly Ala Gly Gly Tyr Gly Gly Gln Gly
385 390 395 400

Gly Tyr Gly Ala Gly Ala Gly Ala Gly Ala Ala Ala Ala Ala Gly Ala
405 410 415

Gly Ala Gly Gly Ala Gly Gly Tyr Gly Arg Gly Ala Gly Ala Gly Ala
420 425 430

Gly Ala Ala Ala Gly Ala Gly Ala Gly Gly Tyr Gly Gly Gln Gly Gly
435 440 445

```
Tyr Gly Ala Gly Ala Gly Ala Gly Ala Ala Ala Ala Ala Ala Thr Gly
    450                 455                 460

Ala Gly Gly Ala Gly Gly Tyr Gly Arg Gly Ala Gly Ala Gly Ala Gly
465                 470                 475                 480

Ala Ala Ala Gly Ala Gly Ala Gly Thr Gly Gly Ala Gly Tyr Gly Gly
                485                 490                 495

Gln Gly Gly Tyr Gly Ala Gly Ala Gly Ala Gly Ala Ala Ala Ala Ala
            500                 505                 510

Gly Ala Gly Ala Gly Gly Ala Gly Tyr Gly Arg Gly Ala Gly Ala Gly
        515                 520                 525

Ala Gly Ala Ala Ala Gly Ala Gly Ala Gly Ala Ala Ala Gly Ala Gly
    530                 535                 540

Ala Gly Ala Gly Gly Tyr Gly Gly Gln Gly Gly Tyr Gly Ala Gly Ala
545                 550                 555                 560

Arg Ala Gly Ala Ala Ala Ala Ala Gly Ala Gly Ala Gly Gly Ala Ala
                565                 570                 575

Gly Tyr Ser Arg Gly Gly Arg Ala Gly Ala Ala Gly Ala Gly Ala Gly
            580                 585                 590

Ala Ala Ala Gly Ala Gly Ala Gly Ala Gly Gly Tyr Gly Gly Gln Gly
        595                 600                 605

Gly Tyr Gly Ala Gly Ala Gly Ala Gly Ala Ala Ala Ala Ala Gly Ala
    610                 615                 620

Gly Ser Gly Gly Ala Gly Gly Tyr Gly Arg Gly Ala Gly Ala Gly Ala
625                 630                 635                 640

Ala Ala Gly Ala Gly Ala Ala Ala Gly Ala Gly Ala Gly Ala Gly Gly
                645                 650                 655

Tyr Gly Gly Gln Gly Gly Tyr Gly Ala Gly Ala Gly Ala Ala Ala Ala
            660                 665                 670

Ala Gly Ala Gly Ala Gly Arg Gly Gly Tyr Gly Arg Gly Ala Gly Ala
        675                 680                 685

Gly Gly Tyr Gly Gly Gln Gly Gly Tyr Gly Ala Gly Ala Gly Ala Gly
    690                 695                 700

Ala Ala Ala Ala Ala Gly Ala Gly Ala Gly Gly Tyr Gly Asp Lys Glu
705                 710                 715                 720

Ile Ala Cys Trp Ser Arg Cys Arg Tyr Thr Val Ala Ser Thr Thr Ser
                725                 730                 735

Arg Leu Ser Ser Ala Glu Ala Ser Ser Arg Ile Ser Ser Ala Ala Ser
            740                 745                 750

Thr Leu Val Ser Gly Gly Tyr Leu Asn Thr Ala Ala Leu Pro Ser Val
        755                 760                 765

Ile Ser Asp Leu Phe Ala Gln Val Gly Ala Ser Ser Pro Val Ile Arg
    770                 775                 780

Gln Arg Ser Leu Ile Gln Val Leu Leu Glu Ile Val Ser Ser Leu Ile
785                 790                 795                 800

His Ile Leu Ser Ser Ser Ser Val Gly Gln Val Asp Phe Ser Ser Val
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805 810 815

Gly Ser Ser Ala Ala Ala Val Gly Gln Ser Met Gln Val Val Met Gly
820 825 830

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 309 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: N. clavipes
(F) TISSUE TYPE: minor ampullate gland

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..309
(D) OTHER INFORMATION: /product= "amino terminus of MISP2 protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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 1               5                  10                  15

GGT GCA GGG GCC GGA GGT TTT GGA GCT GGA GCC TCT GCT GGT GTC GGA        96
Gly Ala Gly Ala Gly Gly Phe Gly Ala Gly Ala Ser Ala Gly Val Gly
            20                  25                  30

GCC GGA GCT GGT ACT GTA GCA GGA TAT GGT GGA CAA GGA GGA TAT GGT       144
Ala Gly Ala Gly Thr Val Ala Gly Tyr Gly Gly Gln Gly Gly Tyr Gly
        35                  40                  45

GCC GGA AGC GCT GGA GGT TAT GGA AGA GGT ACT GGA GCT GGA GCC GCT       192
Ala Gly Ser Ala Gly Gly Tyr Gly Arg Gly Thr Gly Ala Gly Ala Ala
    50                  55                  60

GCT GGT GCC GGA GCA GGA GCC ACT GCT GGT GCC GGA GCA GGA GCC GCT       240
Ala Gly Ala Gly Ala Gly Ala Thr Ala Gly Ala Gly Ala Gly Ala Ala
65                  70                  75                  80

GCT GGT GCC GGA GCA GGA GCA GGT AAT TCA GGA GGA TAT AGT GCC GGA       288
Ala Gly Ala Gly Ala Gly Ala Gly Asn Ser Gly Gly Tyr Ser Ala Gly
                85                  90                  95

GTA GGA GTT GGT GCT GCA GCT                                          309
Val Gly Val Gly Ala Ala Ala
            100
```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 103 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
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 1               5                  10                  15

Gly Ala Gly Ala Gly Gly Phe Gly Ala Gly Ala Ser Ala Gly Val Gly
            20                  25                  30

Ala Gly Ala Gly Thr Val Ala Gly Tyr Gly Gly Gln Gly Gly Tyr Gly
        35                  40                  45

Ala Gly Ser Ala Gly Gly Tyr Gly Arg Gly Thr Gly Ala Gly Ala Ala
    50                  55                  60

Ala Gly Ala Gly Ala Gly Ala Thr Ala Gly Ala Gly Ala Gly Ala Ala
65                  70                  75                  80

Ala Gly Ala Gly Ala Gly Ala Gly Asn Ser Gly Gly Tyr Ser Ala Gly
                85                  90                  95

Val Gly Val Gly Ala Ala Ala
            100
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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 165 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: N. clavipes
(F) TISSUE TYPE: minor ampullate gland

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 3..164
(D) OTHER INFORMATION: /product= "an internal portion of MISP2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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CT GCA GCT GCT GGA GGA GGT GCC GGA ACT GTT GGA GGT TAC GGA AGA          47
   Ala Ala Ala Gly Gly Gly Ala Gly Thr Val Gly Gly Tyr Gly Arg
    1               5                  10                  15

GGT GCT GGT GTA GGA GCA GGT GCC GCT GCT GGT TTT GCG GCA GGA GCT         95
Gly Ala Gly Val Gly Ala Gly Ala Ala Ala Gly Phe Ala Ala Gly Ala
                20                  25                  30

GGT GGT GCT GGA GGC TAC AGA AGA GAT GGA GGA TAC GGT GCT GGA GCA        143
Gly Gly Ala Gly Gly Tyr Arg Arg Asp Gly Gly Tyr Gly Ala Gly Ala
            35                  40                  45

GGA GCT GGA GCT GCT GCA GCT G                                          165
Gly Ala Gly Ala Ala Ala Ala
        50
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(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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Ala Gly Val Gly Ala Gly Ala Ala Ala Gly Phe Ala Ala Gly Ala Gly
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Ala Gly Ala Ala Ala Ala
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(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 870 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: N. clavipes
(F) TISSUE TYPE: minor ampullate gland

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..753
(D) OTHER INFORMATION: /product= "MISP2 carboxy terminus"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

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GCA GGT GCA GAT GCT GGT GGC TAT GGA AGA AAT TAT GGT GCT GGA ACC        96
Ala Gly Ala Asp Ala Gly Gly Tyr Gly Arg Asn Tyr Gly Ala Gly Thr
            20                  25                  30

ACT GCT TAT GCA GGA GCC AGA GCC GGT GGT GCT GGA GGC TAT GGC GGA       144
Thr Ala Tyr Ala Gly Ala Arg Ala Gly Gly Ala Gly Gly Tyr Gly Gly
        35                  40                  45

CAA GGA GGA TAT TCT TCT GGA GCC GGT GCT GCT GCA GCT TCT GGA GCA       192
Gln Gly Gly Tyr Ser Ser Gly Ala Gly Ala Ala Ala Ala Ser Gly Ala
    50                  55                  60

GGA GCC GAT ATC ACT AGT GGA TAC GGA AGA GGT GTT GGT GCT GGA GCT       240
Gly Ala Asp Ile Thr Ser Gly Tyr Gly Arg Gly Val Gly Ala Gly Ala
65                  70                  75                  80
```

```
GGA GCA GAA ACT ATA GGT GCT GGA GGC TAT GGA GGT GGG GCT GGA TCA        288
Gly Ala Glu Thr Ile Gly Ala Gly Gly Tyr Gly Gly Gly Ala Gly Ser
                85                  90                  95

GGA GCA CGT GCG GCT TCA GCA TCC GGA GCT GGT ACT GGA TAT GGT TCG        336
Gly Ala Arg Ala Ala Ser Ala Ser Gly Ala Gly Thr Gly Tyr Gly Ser
            100                 105                 110

TCT GGA GGT TAT AAC GTA GGT ACC GGA ATA AGT ACT TCT TCT GGC GCT        384
Ser Gly Gly Tyr Asn Val Gly Thr Gly Ile Ser Thr Ser Ser Gly Ala
        115                 120                 125

GCA TCT AGC TAC TCT GTT TCT GCT GGA GGT TAT GCT TCA ACA GGT GTT        432
Ala Ser Ser Tyr Ser Val Ser Ala Gly Gly Tyr Ala Ser Thr Gly Val
    130                 135                 140

GGT ATT GGA TCC ACT GTT ACA TCC ACA ACA TCT CGT TTG AGT TCT GCT        480
Gly Ile Gly Ser Thr Val Thr Ser Thr Thr Ser Arg Leu Ser Ser Ala
145                 150                 155                 160

GAA GCA TGT TCT AGA ATA TCT GCT GCG GCT TCC ACT TTA GTA TCT GGA        528
Glu Ala Cys Ser Arg Ile Ser Ala Ala Ala Ser Thr Leu Val Ser Gly
                165                 170                 175

TCC TTG AAT ACT GCA GCT TTA CCA TCT GTA ATT TCG GAT CTT TTT GCC        576
Ser Leu Asn Thr Ala Ala Leu Pro Ser Val Ile Ser Asp Leu Phe Ala
            180                 185                 190

CAA GTT AGT GCA TCA TCA CCC GGG GTA TCA GGT AAC GAA GTT TTG ATT        624
Gln Val Ser Ala Ser Ser Pro Gly Val Ser Gly Asn Glu Val Leu Ile
        195                 200                 205

CAA GTT TTG TTG GAA ATT GTT TCT TCT CTT ATC CAT ATT CTT AGT TCT        672
Gln Val Leu Leu Glu Ile Val Ser Ser Leu Ile His Ile Leu Ser Ser
    210                 215                 220

TCT AGT GTA GGG CAA GTA GAT TTC AGT TCT GTT GGT TCA TCT GCT GCA        720
Ser Ser Val Gly Gln Val Asp Phe Ser Ser Val Gly Ser Ser Ala Ala
225                 230                 235                 240

GCC GTT GGT CAA TCC ATG CAA GTT GTA ATG GGT TAAAACAAAA TGGCTCTCTC      773
Ala Val Gly Gln Ser Met Gln Val Val Met Gly
                245                 250

TCTGTTATAT GCATTCTGTA ATTTCTTCTA AACTATTAAA ATAATGTAAT AATTTCCTGC      833

ATAAATAAAA ATATTTTTCT GCAAAAAAAA AAAAAAA                               870
```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 251 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```
Gly Ala Gly Gly Tyr Gly Arg Gly Ala Gly Ala Gly Ala Ala Ala Val
 1               5                  10                  15

Ala Gly Ala Asp Ala Gly Gly Tyr Gly Arg Asn Tyr Gly Ala Gly Thr
            20                  25                  30

Thr Ala Tyr Ala Gly Ala Arg Ala Gly Gly Ala Gly Gly Tyr Gly Gly
```

```
         35                  40                  45

Gln Gly Gly Tyr Ser Ser Gly Ala Gly Ala Ala Ala Ala Ser Gly Ala
     50                  55                  60

Gly Ala Asp Ile Thr Ser Gly Tyr Gly Arg Gly Val Gly Ala Gly Ala
 65                  70                  75                  80

Gly Ala Glu Thr Ile Gly Ala Gly Gly Tyr Gly Gly Gly Ala Gly Ser
                 85                  90                  95

Gly Ala Arg Ala Ala Ser Ala Ser Gly Ala Gly Thr Gly Tyr Gly Ser
            100                 105                 110

Ser Gly Gly Tyr Asn Val Gly Thr Gly Ile Ser Thr Ser Ser Gly Ala
        115                 120                 125

Ala Ser Ser Tyr Ser Val Ser Ala Gly Gly Tyr Ala Ser Thr Gly Val
    130                 135                 140

Gly Ile Gly Ser Thr Val Thr Ser Thr Thr Ser Arg Leu Ser Ser Ala
145                 150                 155                 160

Glu Ala Cys Ser Arg Ile Ser Ala Ala Ala Ser Thr Leu Val Ser Gly
                165                 170                 175

Ser Leu Asn Thr Ala Ala Leu Pro Ser Val Ile Ser Asp Leu Phe Ala
            180                 185                 190

Gln Val Ser Ala Ser Ser Pro Gly Val Ser Gly Asn Glu Val Leu Ile
        195                 200                 205

Gln Val Leu Leu Glu Ile Val Ser Ser Leu Ile His Ile Leu Ser Ser
    210                 215                 220

Ser Ser Val Gly Gln Val Asp Phe Ser Ser Val Gly Ser Ser Ala Ala
225                 230                 235                 240

Ala Val Gly Gln Ser Met Gln Val Val Met Gly
                245                 250
```

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 165 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: N. clavipes
(F) TISSUE TYPE: minor ampullate gland

(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..165
(D) OTHER INFORMATION: /label= cloned_cDNA
/note= "pMISS3 partial sequence, 11-1 template, forward primer"

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..165

(D) OTHER INFORMATION: /product= "translation of pMISS3 partial sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```
GCT GGA GCT GCT GCT GGT GCT GGA GGC TAT GAC GGA CAA GGA GGA TAT        48
Ala Gly Ala Ala Ala Gly Ala Gly Gly Tyr Asp Gly Gln Gly Gly Tyr
 1               5                  10                  15

GGT GCT GGA GCA GGA GCT GCT GCA GCT GCT GGA GCA GGA GCC GGA AGC        96
Gly Ala Gly Ala Gly Ala Ala Ala Ala Ala Gly Ala Gly Ala Gly Ser
            20                  25                  30

GTT GGA GGT TAT GGA ACA GGT GCT GTA GCT GGA TCT GGA ACA GCT GCT       144
Val Gly Gly Tyr Gly Thr Gly Ala Val Ala Gly Ser Gly Thr Ala Ala
        35                  40                  45

GGT GCA GGA GCC AGA GCT GGT                                          165
Gly Ala Gly Ala Arg Ala Gly
    50                  55
```

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```
Ala Gly Ala Ala Ala Gly Ala Gly Gly Tyr Asp Gly Gln Gly Gly Tyr
 1               5                  10                  15

Gly Ala Gly Ala Gly Ala Ala Ala Ala Ala Gly Ala Gly Ala Gly Ser
            20                  25                  30

Val Gly Gly Tyr Gly Thr Gly Ala Val Ala Gly Ser Gly Thr Ala Ala
        35                  40                  45

Gly Ala Gly Ala Arg Ala Gly
    50                  55
```

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 240 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: N. clavipes
(F) TISSUE TYPE: minor ampullate gland

(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..240
(D) OTHER INFORMATION: /label= cloned_cDNA
/note= "partial sequence of pMISS3, 11-1 template, reverse primer"

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..240
(D) OTHER INFORMATION: /product= "pMISS3 partial sequence translation"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```
GGA GCT GCT GCT GGT GCA GGA GCC GGA GCA GGT AGT ACA GGA GGC TTT        48
Gly Ala Ala Ala Gly Ala Gly Ala Gly Ala Gly Ser Thr Gly Gly Phe
 1               5                  10                  15

GGC GGA CAA GGA GGA TAT GGT GCC GGT GCA GGA GCT GCA GCT GCT GGA        96
Gly Gly Gln Gly Gly Tyr Gly Ala Gly Ala Gly Ala Ala Ala Ala Gly
            20                  25                  30

GCT TTT GCC GGA AGA GCT GGG GGT TAC GGA AGA GCT GCT GGA GCT GCG       144
Ala Phe Ala Gly Arg Ala Gly Gly Tyr Gly Arg Ala Ala Gly Ala Ala
        35                  40                  45

GCT GGA ACT GGA GCT GCT GCT GGT GCA GGA GCC GGA GCT GGT AGT ACA       192
Ala Gly Thr Gly Ala Ala Ala Gly Ala Gly Ala Gly Ala Gly Ser Thr
    50                  55                  60

GGA GGC TTT GGC GGA CAA AGA GGA TAC GGT GCC GGC AGA AGT AAT GGA       240
Gly Gly Phe Gly Gly Gln Arg Gly Tyr Gly Ala Gly Arg Ser Asn Gly
65                  70                  75                  80
```

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```
Gly Ala Ala Ala Gly Ala Gly Ala Gly Ala Gly Ser Thr Gly Gly Phe
 1               5                  10                  15

Gly Gly Gln Gly Gly Tyr Gly Ala Gly Ala Gly Ala Ala Ala Ala Gly
            20                  25                  30

Ala Phe Ala Gly Arg Ala Gly Gly Tyr Gly Arg Ala Ala Gly Ala Ala
        35                  40                  45

Ala Gly Thr Gly Ala Ala Ala Gly Ala Gly Ala Gly Ala Gly Ser Thr
    50                  55                  60

Gly Gly Phe Gly Gly Gln Arg Gly Tyr Gly Ala Gly Arg Ser Asn Gly
65                  70                  75                  80
```

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 144 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: N. clavipes
(F) TISSUE TYPE: minor ampullate gland

(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..144
(D) OTHER INFORMATION: /label= cloned_cDNA
/note= "partial sequence of pMISS3, 11-2 template, forward primer"

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..144
(D) OTHER INFORMATION: /product= "translation of pMISS3 partial sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```
TAT GGT GGA CAA GGC GGA TAT GGT GCT GGA GCA GGA GCT GGT GCT GCT        48
Tyr Gly Gly Gln Gly Gly Tyr Gly Ala Gly Ala Gly Ala Gly Ala Ala
 1               5                  10                  15

GCA GCC GCA GGA TAT GGA GCC GGT GCT GGA GGA TAC GGT GGA CAA GCT        96
Ala Ala Ala Gly Tyr Gly Ala Gly Ala Gly Gly Tyr Gly Gly Gln Ala
            20                  25                  30

GGT TAT GGT GCC GGA GCT GGA GCT GGT AGT TCT GCA GGA AAT GCT TTC       144
Gly Tyr Gly Ala Gly Ala Gly Ala Gly Ser Ser Ala Gly Asn Ala Phe
        35                  40                  45
```

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```
Tyr Gly Gly Gln Gly Gly Tyr Gly Ala Gly Ala Gly Ala Gly Ala Ala
 1               5                  10                  15

Ala Ala Ala Gly Tyr Gly Ala Gly Ala Gly Gly Tyr Gly Gly Gln Ala
            20                  25                  30

Gly Tyr Gly Ala Gly Ala Gly Ala Gly Ser Ser Ala Gly Asn Ala Phe
        35                  40                  45
```

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 155 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..155
(D) OTHER INFORMATION: /label= MISPN_aa
/note= "amino-terminal sequence of mispl, see Fig. 4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Asn Asn Leu Leu Phe Ala Val Ser Gly Tyr Val Ser Thr Leu Gly
1 5 10 15

Asn Ala Ile Ser Asp Ala Ser Ala Tyr Ala Asn Ala Leu Ser Ser Ala
20 25 30

Ile Gly Asn Val Leu Ala Asn Ser Gly Ser Ile Ser Glu Ser Thr Ala
35 40 45

Ser Ser Ala Ala Ser Ser Ala Ala Ser Ser Val Thr Thr Thr Leu Thr
50 55 60

Ser Tyr Gly Pro Ala Val Phe Tyr Ala Pro Ser Ala Ser Ser Gly Gly
65 70 75 80

Tyr Gly Ala Gly Ala Gly Ala Val Ala Ala Ala Gly Ala Ala Gly Ala
85 90 95

Gly Gly Tyr Gly Arg Gly Ala Gly Gly Tyr Gly Gly Gln Gly Gly Tyr
100 105 110

Gly Ala Gly Ala Gly Ala Gly Ala Ala Ala Ala Ala Gly Ala Gly Ala
115 120 125

Gly Gly Ala Gly Gly Tyr Gly Arg Gly Ala Gly Ala Gly Ala Gly Ala
130 135 140

Ala Ala Gly Ala Gly Ala Gly Ala Gly Gly Ala
145 150 155

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..90
(D) OTHER INFORMATION: /label= MISP2N_AA
/note= "amino terminal peptide of MISP2, see Fig. 4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ser Tyr Gly Pro Ser Val Phe Tyr Thr Pro Thr Ser Ala Gly Ser Tyr
1 5 10 15

Gly Ala Gly Ala Gly Ala Phe Gly Ala Gly Ala Ser Ala Gly Val Gly
20 25 30

Ala Gly Ala Gly Thr Val Ala Gly Tyr Gly Gly Gln Gly Gly Tyr Gly
35 40 45

Ala Gly Ala Gly Ser Ala Gly Gly Tyr Gly Arg Gly Thr Gly Ala Gly
50 55 60

Ala Ala Ala Gly Ala Gly Ala Gly Ala Thr Ala Gly Ala Gly Ala Gly
65 70 75 80

Ala Ala Ala Gly Ala Gly Ala Gly Ala Gly
85 90

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: C-terminal

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..115
(D) OTHER INFORMATION: /label= MISP1C_AA
/note= "carboxyl terminus of MISP1, see Fig. 4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Asp Lys Glu Ile Ala Cys Trp Ser Arg Cys Arg Tyr Thr Val Ala Ser
1 5 10 15

Thr Thr Ser Arg Leu Ser Ser Ala Glu Ala Ser Ser Arg Ile Ser Ser
20 25 30

Ala Ala Ser Thr Leu Val Ser Gly Gly Tyr Leu Asn Thr Ala Ala Leu
35 40 45

Pro Ser Val Ile Ser Asp Leu Phe Ala Gln Val Gly Ala Ser Ser Pro
50 55 60

Val Ile Arg Gln Arg Ser Leu Ile Gln Val Leu Leu Glu Ile Val Ser
65 70 75 80

Ser Leu Ile His Ile Leu Ser Ser Ser Ser Val Gly Trp Val Asp Phe
85 90 95

Ser Ser Val Gly Ser Ser Ala Ala Ala Val Gly Gln Ser Met Gln Val
100 105 110

Val Met Gly
115

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: C-terminal

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..116
(D) OTHER INFORMATION: /label= MISP2C_AA
/note= "carboxyl terminus of MISP2, see Fig. 4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Gly Gly Tyr Ala Ser Thr Gly Val Gly Ile Gly Ser Thr Val Thr Ser
1 5 10 15

Thr Thr Ser Arg Leu Ser Ser Ala Glu Ala Cys Ser Arg Ile Ser Ala
20 25 30

Ala Ala Ser Thr Leu Val Ser Gly Gly Ser Leu Asn Thr Ala Ala Leu
35 40 45

Pro Ser Val Ile Ser Asp Leu Phe Ala Gln Val Ser Ala Ser Ser Pro
50 55 60

Gly Val Ser Gly Asn Glu Val Leu Ile Gln Val Leu Leu Glu Ile Val
65 70 75 80

Ser Ser Leu Ile His Ile Leu Ser Ser Ser Ser Val Gly Gln Val Asp
85 90 95

Phe Ser Ser Val Gly Ser Ser Ala Ala Ala Val Gly Gln Ser Met Gln
100 105 110

Val Val Met Gly
115

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..33
(D) OTHER INFORMATION: /label= mispl_repeat
/note= "see Table 1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Gly Ala Ala Gly Ala Gly Gly Tyr Gly Arg Gly Ala Gly Gly Tyr Gly
1 5 10 15

Gly Gln Gly Gly Tyr Gly Ala Gly Ala Gly Ala Gly Ala Ala Ala Ala
20 25 30

Ala

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..51
(D) OTHER INFORMATION: /label= misp1_repeat
/note= "see Table 1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Gly Ala Gly Ala Gly Gly Ala Gly Gly Tyr Gly Arg Gly Ala Gly Ala
1 5 10 15

Gly Ala Gly Ala Ala Ala Gly Ala Gly Ala Gly Ala Gly Gly Ala Gly
20 25 30

Tyr Gly Gly Gln Gly Gly Tyr Gly Ala Gly Ala Gly Ala Gly Ala Ala
35 40 45

Ala Ala Ala
50

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..48
(D) OTHER INFORMATION: /label= misp1_repeat
/note= "see Table 1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Gly Ala Gly Ala Gly Gly Ala Gly Gly Tyr Gly Arg Gly Ala Gly Ala
1 5 10 15

Gly Ala Gly Ala Ala Ala Gly Ala Gly Ala Gly Gly Tyr Gly Gly Gln
20 25 30

Gly Gly Tyr Gly Ala Gly Ala Gly Ala Gly Ala Ala Ala Ala Ala Ala
35 40 45

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..49
(D) OTHER INFORMATION: /label= mispl_repeat
/note= "see Table 1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Gly Ala Gly Ser Gly Gly Ala Gly Gly Tyr Gly Arg Gly Ala Gly Ala
1 5 10 15

Gly Ala Gly Ala Ala Ala Gly Ala Gly Ala Gly Ala Gly Ser Tyr Gly
20 25 30

Gly Gln Gly Gly Tyr Gly Ala Gly Ala Gly Ala Gly Ala Ala Ala Ala
35 40 45

Ala

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..39
(D) OTHER INFORMATION: /label= mispl_repeat
/note= "see Table 1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Gly Ala Gly Ala Gly Gly Ala Gly Gly Tyr Gly Arg Gly Ala Gly Ala
1 5 10 15

Gly Ala Gly Ala Gly Ala Gly Ala Ala Ala Arg Ala Gly Ala Gly Ala
20 25 30

Gly Gly Ala Ala Ala Ala Ala
35

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..47
(D) OTHER INFORMATION: /label= misp1_repeat
/note= "see Table 1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Gly Ala Gly Ala Gly Gly Ala Gly Gly Tyr Gly Arg Gly Ala Gly Ala
1 5 10 15

Gly Ala Gly Ala Ala Ala Gly Ala Gly Ala Gly Ala Gly Gly Tyr Gly
20 25 30

Gly Gln Ser Gly Tyr Gly Ala Gly Ala Gly Ala Ala Ala Ala Ala
35 40 45

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..55
(D) OTHER INFORMATION: /label= misp1_repeat
/note= "see Table 1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Gly Ala Gly Ala Gly Gly Ala Gly Gly Tyr Gly Arg Gly Ala Gly Ala
1 5 10 15

Gly Ala Gly Ala Ala Ala Gly Ala Gly Ala Gly Ala Ala Ala Gly Ala
20 25 30

Gly Ala Gly Gly Tyr Gly Gly Gln Gly Gly Tyr Gly Ala Gly Ala Gly
35 40 45

Ala Gly Ala Ala Ala Ala Ala
50 55

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..47
(D) OTHER INFORMATION: /label= misp1_repeat

/note= "see Table 1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Gly Ala Gly Ala Gly Gly Ala Gly Gly Tyr Gly Arg Gly Ala Gly Ala
1 5 10 15

Gly Ala Gly Ala Ala Ala Gly Ala Gly Ala Gly Gly Tyr Gly Gly Gln
20 25 30

Gly Gly Tyr Gly Ala Gly Ala Gly Ala Gly Ala Ala Ala Ala Ala
35 40 45

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..50
(D) OTHER INFORMATION: /label= mispl_repeat
/note= "see Table 1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Thr Gly Ala Gly Gly Ala Gly Gly Tyr Gly Arg Gly Ala Gly Ala Gly
1 5 10 15

Ala Gly Ala Ala Ala Gly Ala Gly Ala Gly Thr Gly Gly Ala Gly Tyr
20 25 30

Gly Gly Gln Gly Gly Tyr Gly Ala Gly Ala Gly Ala Gly Ala Ala Ala
35 40 45

Ala Ala
50

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..56
(D) OTHER INFORMATION: /label= mispl_repeat
/note= "see Table 1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Gly Ala Gly Ala Gly Gly Ala Gly Tyr Gly Arg Gly Ala Gly Ala Gly
1 5 10 15

Ala Gly Ala Ala Ala Gly Ala Gly Ala Gly Ala Ala Ala Gly Ala Gly
20 25 30

Ala Gly Ala Gly Gly Tyr Gly Gly Gln Gly Gly Tyr Gly Ala Gly Ala
35 40 45

Arg Ala Gly Ala Ala Ala Ala Ala
50 55

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..54
(D) OTHER INFORMATION: /label= misp1_repeat
/note= "see Table 1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Gly Ala Gly Ala Gly Gly Ala Ala Gly Tyr Ser Arg Gly Gly Arg Ala
1 5 10 15

Gly Ala Ala Gly Ala Gly Ala Gly Ala Ala Ala Gly Ala Gly Ala Gly
20 25 30

Ala Gly Gly Tyr Gly Gly Gln Gly Gly Tyr Gly Ala Gly Ala Gly Ala
35 40 45

Gly Ala Ala Ala Ala Ala
50

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..51
(D) OTHER INFORMATION: /label= misp1_repeat
/note= "see Table 1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Gly Ala Gly Ser Gly Gly Ala Gly Gly Tyr Gly Arg Gly Ala Gly Ala

```
1               5                   10                  15

Gly Ala Ala Ala Gly Ala Gly Ala Ala Ala Gly Ala Gly Ala Gly Ala
            20                  25                  30

Gly Gly Tyr Gly Gly Gln Gly Gly Tyr Gly Ala Gly Ala Gly Ala Ala
        35                  40                  45

Ala Ala Ala
    50
```

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: C-terminal

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..36
(D) OTHER INFORMATION: /label= misp1_repeat
/note= "see Table 1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

```
Gly Ala Gly Ala Gly Arg Gly Gly Tyr Gly Arg Gly Ala Gly Ala Gly
1               5                   10                  15

Gly Tyr Gly Gly Gln Gly Gly Tyr Gly Ala Gly Ala Gly Ala Gly Ala
            20                  25                  30

Ala Ala Ala Ala
        35
```

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..55
(D) OTHER INFORMATION: /label= misp1_repeat
/note= "consensus sequence of MiSP1 repeats"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```
Arg Gly Ala Ala Gly Ala Ala Gly Ala Gly Ala Gly Ala Ala Ala Gly
1               5                   10                  15

Ala Gly Ala Gly Ala Gly Ala Gly Gly Tyr Gly Gly Gln Gly Gly Tyr
            20                  25                  30
```

Gly Ala Gly Ala Gly Ala Gly Ala Ala Ala Ala Ala Gly Ala Gly Ala
35 40 45

Gly Gly Ala Gly Gly Tyr Gly
50 55

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..11
(D) OTHER INFORMATION: /label= misp1_generic
/note= "generic formula for MiSP1"

(ix) FEATURE:
(A) NAME/KEY: Duplication
(B) LOCATION: 3..4
(D) OTHER INFORMATION: /label= GA
/note= "(GA) repeated 1 to 6 times"

(ix) FEATURE:
(A) NAME/KEY: Duplication
(B) LOCATION: 5
(D) OTHER INFORMATION: /label= A
/note= "present as 0 to 4 residues"

(ix) FEATURE:
(A) NAME/KEY: Duplication
(B) LOCATION: 6..8
(D) OTHER INFORMATION: /label= GGX
/note= "X is tyrosine, glutamine or alanine; unit is repeated 1 to 4 times."

(ix) FEATURE:
(A) NAME/KEY: Duplication
(B) LOCATION: 9..10
(D) OTHER INFORMATION: /label= GA
/note= "repeated 1 to 6 times"

(ix) FEATURE:
(A) NAME/KEY: Duplication
(B) LOCATION: 11
(D) OTHER INFORMATION: /label= A
/note= "present as 0 to 4 residues"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Gly Arg Gly Ala Ala Gly Gly Xaa Gly Ala Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..15
(D) OTHER INFORMATION: /label= MaSP1_generic
/note= "generic formula for MaSP1 protein (major ampullate spider silk protein)."

(ix) FEATURE:
(A) NAME/KEY: Duplication
(B) LOCATION: 1..3
(D) OTHER INFORMATION: /label= XGG
/note= "X is tyrosine or glutamine; unit is repeated 2 to 3 times"

(ix) FEATURE:
(A) NAME/KEY: Region
(B) LOCATION: 4..6
(D) OTHER INFORMATION: /label= XGA
/note= "X is tyrosine or glutamine; unit is present once."

(ix) FEATURE:
(A) NAME/KEY: Duplication
(B) LOCATION: 7..9
(D) OTHER INFORMATION: /label= GXG
/note= "X is tyrosine or glutamine; unit is repeated 1 to three times."

(ix) FEATURE:
(A) NAME/KEY: Duplication
(B) LOCATION: 10..12
(D) OTHER INFORMATION: /label= AGA
/note= "unit is repeated 5 to 7 times"

(ix) FEATURE:
(A) NAME/KEY: Duplication
(B) LOCATION: 13
(D) OTHER INFORMATION: /label= G
/note= "present as 1 or 2 residues"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Xaa Gly Gly Xaa Gly Ala Gly Xaa Gly Ala Gly Ala Gly Ala Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..14
(D) OTHER INFORMATION: /label= MaSP2_generic

/note= "generic formula for MaSP2 protein (major ampullate spider silk protein)."

(ix) FEATURE:
(A) NAME/KEY: Duplication
(B) LOCATION: 1..10
(D) OTHER INFORMATION: /label= GPG2YGPGQ2
/note= "unit is repeated 2 or 3 times"

(ix) FEATURE:
(A) NAME/KEY: Duplication
(B) LOCATION: 11..12
(D) OTHER INFORMATION: /label= XX
/note= "X is GPG or GPS"

(ix) FEATURE:
(A) NAME/KEY: Duplication
(B) LOCATION: 14
(D) OTHER INFORMATION: /label= A
/note= "present as 7 to 10 residues"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Gly Pro Gly Gly Tyr Gly Pro Gly Gln Gln Xaa Xaa Ser Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..6
(D) OTHER INFORMATION: /label= MiSP_simple
/note= "simplified MiSP1 generic formula; x is tyrosine, glutamine or alan..."

(ix) FEATURE:
(A) NAME/KEY: Duplication
(B) LOCATION: 1..3
(D) OTHER INFORMATION: /label= GGX
/note= "X is tyrosine, glutamine or alanine; unit is repeated 1 to 4 times."

(ix) FEATURE:
(A) NAME/KEY: Duplication
(B) LOCATION: 4..5
(D) OTHER INFORMATION: /label= GA
/note= "unit is present 0 to 4 times"

(ix) FEATURE:
(A) NAME/KEY: Duplication
(B) LOCATION: 6
(D) OTHER INFORMATION: /label= A
/note= "present as 1 to 6 residues"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

```
Gly Gly Xaa Gly Ala Ala
1               5
```

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..47
(D) OTHER INFORMATION: /label= MaSP2_repeat
/note= "see Table 2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

```
Gly Pro Gly Gln Gln Gly Pro Gly Gly Tyr Gly Pro Gly Gln Gln Gly
1               5                   10                  15

Pro Ser Gly Pro Gly Ser Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala
            20                  25                  30

Gly Pro Gly Gly Tyr Gly Pro Gly Gln Gln Gly Pro Gly Gly Tyr
        35                  40                  45
```

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..38
(D) OTHER INFORMATION: /label= MaSP2_repeat
/note= "see Table 2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```
Gly Pro Gly Gln Gln Gly Pro Gly Arg Tyr Gly Pro Gly Gln Gln Gly
1               5                   10                  15

Pro Ser Gly Pro Gly Ser Ala Ala Ala Ala Ala Ala Gly Ser Gly Gln
            20                  25                  30

Gln Gly Pro Gly Gly Tyr
        35
```

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..52
(D) OTHER INFORMATION: /label= MaSP2_repeat
/note= "see Table 2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Gly Pro Arg Gln Gln Gly Pro Gly Gly Tyr Gly Gln Gly Gln Gln Gly
1 5 10 15

Pro Ser Gly Pro Gly Ser Ala Ala Ala Ala Ser Ala Ala Ala Ser Ala
20 25 30

Glu Ser Gly Gln Gln Gly Pro Gly Gly Tyr Gly Pro Gly Gln Gln Gly
35 40 45

Pro Gly Gly Tyr
50

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..40
(D) OTHER INFORMATION: /label= MaSP2_repeat
/note= "see Table 2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Gly Pro Gly Gln Gln Gly Pro Gly Gly Tyr Gly Pro Gly Gln Gln Gly
1 5 10 15

Pro Ser Gly Pro Gly Ser Ala Ala Ala Ala Ala Ala Ala Ser Gly Pro
20 25 30

Gly Gln Gln Gly Pro Gly Gly Tyr
35 40

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..41
(D) OTHER INFORMATION: /label= MaSP2_repeat
/note= "see Table 2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

```
Gly Pro Gly Gln Gln Gly Pro Gly Gly Tyr Gly Pro Gly Gln Gln Gly
1               5                  10                  15

Pro Ser Gly Pro Gly Ser Ala Ala Ala Ala Ala Ala Ala Ala Ser Gly
            20                  25                  30

Pro Gly Gln Gln Gly Pro Gly Gly Tyr
        35                  40
```

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..29
(D) OTHER INFORMATION: /label= MaSP2_repeat
/note= "see Table 2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

```
Gly Pro Gly Gln Gln Gly Pro Gly Gly Tyr Gly Pro Gly Gln Gln Gly
1               5                  10                  15

Leu Ser Gly Pro Gly Ser Ala Ala Ala Ala Ala Ala Ala
            20                  25
```

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..36
(D) OTHER INFORMATION: /label= MaSP2_repeat
/note= "see Table 2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Gly Pro Gly Gln Gln Gly Pro Gly Gly Tyr Gly Pro Gly Gln Gln Gly
1 5 10 15

Pro Ser Gly Pro Gly Ser Ala Ala Ala Ala Ala Ala Ala Ala Gly
20 25 30

Pro Gly Gly Tyr
35

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..39
(D) OTHER INFORMATION: /label= MaSP2_repeat
/note= "see Table 2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Gly Pro Gly Gln Gln Gly Pro Gly Gly Tyr Gly Pro Gly Gln Gln Gly
1 5 10 15

Pro Ser Gly Ala Gly Ser Ala Ala Ala Ala Ala Ala Ala Gly Pro Gly
20 25 30

Gln Gln Gly Leu Gly Gly Tyr
35

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..32
(D) OTHER INFORMATION: /label= MaSP2_repeat
/note= "see Table 2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Gly Pro Gly Gln Gln Gly Pro Gly Gly Tyr Gly Pro Gly Gln Gln Gly
1 5 10 15

Pro Gly Gly Tyr Gly Pro Gly Ser Ala Ser Ala Ala Ala Ala Ala Ala
20 25 30

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..37
(D) OTHER INFORMATION: /label= MaSP2_repeat
/note= "see Table 2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Gly Pro Gly Gln Gln Gly Pro Gly Gly Tyr Gly Pro Gly Gln Gln Gly
1 5 10 15

Pro Ser Gly Pro Gly Ser Ala Ser Ala Ala Ala Ala Ala Ala Ala Ala
20 25 30

Gly Pro Gly Gly Tyr
35

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..37
(D) OTHER INFORMATION: /label= MaSP2_repeat
/note= "see Table 2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Gly Pro Gly Gln Gln Gly Pro Gly Gly Tyr Ala Pro Gly Gln Gln Gly
1 5 10 15

Pro Ser Gly Pro Gly Ser Ala Ser Ala Ala Ala Ala Ala Ala Ala Ala
20 25 30

Gly Pro Gly Gly Tyr
35

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: C-terminal

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..36
(D) OTHER INFORMATION: /label= MaSP2_repeat
/note= "see Table 2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

```
Gly Pro Gly Gln Gln Gly Pro Gly Gly Tyr Ala Pro Gly Gln Gln Gly
1               5                   10                  15

Pro Ser Gly Pro Gly Ser Ala Ala Ala Ala Ala Ala Ala Ser Ala Gly
            20                  25                  30

Pro Gly Gly Tyr
        35
```

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..37
(D) OTHER INFORMATION: /label= MaSP2_consensus
/note= "consensus sequence of MaSP2 repeat units"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

```
Gly Pro Gly Gln Gln Gly Pro Gly Gly Tyr Gly Pro Gly Gln Gln Gly
1               5                   10                  15

Pro Ser Gly Pro Gly Ser Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala
            20                  25                  30

Gly Pro Gly Gly Tyr
        35
```

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..84
(D) OTHER INFORMATION: /label= oligonucleotide
/note= "S2 long oligo"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TCTAGCCCGG GTGGCTATGG TCCTGGACAG CAAGGTCCTG GCGGTTACGG TCCTGGCCAA 60

CAGGGTCCCT CTGGTCCAGG CAGT 84

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..59
(D) OTHER INFORMATION: /label= oligonucleotide
/note= "S2 short oligo"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TCCGGACCTG CTGCGGCGGC TGCGGCAGCT GCACTGCCTG GACCAGAGGG ACCCTGTTG 59

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..35
(D) OTHER INFORMATION: /label= MaSP2_repeat
/note= "basic repeat unit of MaSP2 protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Pro Gly Gly Tyr Gly Pro Gly Gln Gln Gly Pro Gly Gly Tyr Gly Pro
1 5 10 15

Gly Gln Gln Gly Pro Ser Gly Pro Gly Ser Ala Ala Ala Ala Ala Ala
20 25 30

Ala Ala Gly
35

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..13
(D) OTHER INFORMATION: /label= enzyme_site
/note= "generic recognition site for Sfi I restriction enzyme"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GGCCNNNNNG GCC 13

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..13
(D) OTHER INFORMATION: /label= Sfi_I_site
/note= "top strand of synthetic Sfi I/AlwN I linker"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GGCCGCAGCG GCC 13

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..4
(D) OTHER INFORMATION: /label= linker_peptide
/note= "amino acids encoded by Sfi I/AlwN I linker"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ala Ala Ala Ala
1

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..6
(D) OTHER INFORMATION: /label= NBS_peptides
/note= "see discussion page 13"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Gly Gly Gln Gly Gly Tyr
1 5

CLAIMS

What is claimed is:

1. A polypeptide having an amino acid sequence comprising repeats of the unit amino acid sequence RGAAGAAGAGAGAAAGAGAGAGAGGYGGQGGYGAGAGAGAAAAAGAGAGGAGGYG.

2. A polypeptide having the amino acid sequence shown in Figure 1.

3. A polypeptide comprising one or more repeats of a unit amino acid repeat sequence selected from the group consisting of GAAGAGGYGRGAGGYGGQGGYGAGAGAGAAAAA, GAGAGGAGGYGRGAGAGAGAAAGAGAGAGGAGYGGQGGYGAGAGAGAAAAA, GAGAGGAGGYGRGAGAGAGAAAGAGAGGYGGQGGYGAGAGAGAAAAAA, GAGSGGAGGYGRGAGAGAGAAAGAGAGAGSYGGQGGYGAGAGAGAAAAA, GAGAGGAGGYGRGAGAGAGAGAGAAARAGAGAGGAAAAA, GAGAGGAGGYGRGAGAGAGAGAGAAARAGAGAGG, GAGAGGAGGYGRGAGAGAGAAAGAGAGAGGYGGQSGYGAGAGAAAAA, GAGAGGAGGYGRGAGAGAGAAAGAGAGAAAGAGAGGYGGQGGYGAGAGAGAAAAA, GAGAGGAGGYGRGAGAGAGAAAGAGAGGYGGQGGYGAGAGAGAAAAA, TGAGGAGGYGRGAGAGAGAAAGAGAGTGGAGYGGQGGYGAGAGAGAAAAA, GAGAGGAGYGRGAGAGAGAAAGAGAGAAAGAGAGAGGYGGQG GYGAGARAGAAAAA, GAGAGGAAGYSRGGRAGAAGAGAGAAAGAGAGAGGYGGQGGYGAGAGAGAAAAA, GAGSGGAGGYGRGAGAGAAAGAGAAAGAGAGAGGYGGQGGYGAGAGAAAAA, and GAGAGRGGYGRGAGAGGYGGQGGYGAGAGAGAAAAA.

4. A polypeptide according to claim 3, wherein all repeats are of the same unit amino acid repeat sequence.

5. A polypeptide according to claim 3 further comprising an amino terminal polypeptide having the amino acid sequence
N N L L F A V S G Y V S T L G N A I S D A S A Y A N A L S S A I G N V L A N S G S I S E S T A S S A A S S A A S S V T T T
L T S Y G P A V F Y A P S A S S G G Y G A G A G A V A A A G A A G A G G Y G R G A G G Y G G Q G G Y G A G A G A G A A A A G A G A G G A G G Y G R G A G A G A G A A A G A G A G A G G A.

6. A polypeptide according to claim 3 further comprising an amino terminal polypeptide having the amino acid sequence
S Y G P S V F Y T P T S A G S Y G A G A G A F G A G A S A G V G A G A G T V A G Y G G Q G G Y G A G A G S A G G Y G R G T G A G A A A G A G A G A T A G A G A G A A A G A G A G A G A G.

7. A polypeptide according to claim 3 further comprising a carboxy terminal polypeptide having the amino acid sequence
D K E I A C W S R C R Y T V A S T T S R L S S A E A S S R I S S A A S T L V S G G Y L N T A A L P S V I S D L F A Q V G A S
S P V I R Q R S L I Q V L L E I V S S L I H I L S S S S V G W V D F S S V G S S A A A V G Q S M Q V V M G.

8. A polypeptide according to claim 3 further comprising a carboxy terminal polypeptide having the amino acid sequence
G G Y A S T G V G I G S T V T S T T S R L S S A E A C S R I S A A A S T L V S G G S L N T A A L P S V I S D L F A Q V S A S S P G V S G N E V L I Q V L L E I V S S L I H I L S S S S V G Q V D F S S V G S S A A A V G Q S M Q V V M G.

9. A polypeptide according to claim 5 further comprising a carboxy terminal polypeptide having the amino acid sequence
D K E I A C W S R C R Y T V A S T T S R L S S A E A S S
R I S S A A S T L V S G G Y L N T A A L P S V I S D L F
A Q V G A S
S P V I R Q R S L I Q V L L E I V S S L I H I L S S S S
V G W V D F S S V G S S A A A V G Q S M Q V V M G.

10. A polypeptide according to claim 5 further comprising a carboxy terminal polypeptide having the amino acid sequence
G G Y A S T G V G I G S T V T S T T S R L S S A E A C S
R I S A A A S T L V S G G S L N T A A L P S V I S D L F
A Q V S A S S P G V S G N E V L I Q V L L E I V S S L I
H I L S S S S V G Q V D F S S V G S S A A A V G Q S M Q
V V M G.

11. An isolated DNA molecule encoding a polypeptide of any one of claims 1, 3 and 10.

12. An isolated DNA molecule having the nucleotide sequence of Figure 1.

13. A fiber comprising an aggregate of polypeptides according to any one of claims 1 through 10.

14. A fiber comprising an aggregate of polypeptides according to claim 7 and polypeptides according to claim 8.

15. A fiber comprising an aggregate of polypeptides according to claim 9 and polypeptides according to claim 10.

16. A host cell transformed with a DNA according to any one of claim 11.

17. A host cell transformed with a DNA according to claim 12.

18. A polypeptide comprising repeats of an amino acid sequence having the generic formula

$$(GR)(GA)_l(A)_m(GGX)_n(GA)_l(A)_m$$

where X is tyrosine, glutamine or alanine and where l = 1 to 6, m = 0 to 4 and n = 1 to 4.

19. An isolated DNA molecule encoding a polypeptide of claim 18.

20. A host cell transformed with a DNA molecule according to claim 19.

21. A polypeptide comprising repeats of an amino acid sequence having the generic formula:

$$(GGX)_n(GA)_m(A)_l$$

where X is tyrosine, glutamine or alanine and where l = 1 to 6, m = 0 to 4 and n = 1 to 4.

22. An isolated DNA molecule encoding a polypeptide of claim 21.

23. A host cell transformed with a DNA molecule according to claim 22.

24. An isolated DNA molecule comprising a polynucleotide that will hybridize to a DNA molecule having the sequence of Figure 1A-1F under conditions obtained by a solution of 6X SSC or SSPE, 5X Denhardt's solution, 0.5% SDS at a temperature of about 68°C, or under conditions obtained by the said solution that is made 50% in formamide at a temperature of about 42°C.

```
         10          20          30          40          50
    *    *    *    *    *    *    *    *    *    *
ACATA CTAGG TTTGG TGCCG GAGCT GGAGC TGGTA CGTCT GTGCA GAAAT

         60          70          80          90         100
    *    *    *    *    *    *    *    *    *    *
ACTTT GCACA TCACT TCTCC AATTG CTTCT CGGGT ATTTG TCAAA TGATT

        110         120         130         140         150
    *    *    *    *    *    *    *    *    *    *
AGTTC TACAA CTTCT ACTGA TCATG CAGTA AGTGT TGCTA CGAGC GTTGC

        160         170         180         190
    *    *    *    *    *    *    *    *    *
GCTGA AGTCA GCTTG GACTT GATGC AAATG CT ATG AAC AAC TTA CTA
                                      M   N   N   L   L>

200         210         220         230         240
  *    *    *    *    *    *    *    *    *    *
GGT GCC GTT AGT GGA TAT GTT TCG ACA CTA GGC AAC GCT ATT TCT
 G   A   V   S   G   Y   V   S   T   L   G   N   A   I   S>

       250         260         270         280
  *    *    *    *    *    *    *    *    *    *
GAT GCT TCG GCA TAC GCA AAT GCT CTT TCT TCC GCT ATA GGA AAT
 D   A   S   A   Y   A   N   A   L   S   S   A   I   G   N>

290         300         310         320         330
  *    *    *    *    *    *    *    *    *    *
GTG TTA GCT AAT TCC GGT TCA ATT AGC GAA AGC ACT GCA TCT TCT
 V   L   A   N   S   G   S   I   S   E   S   T   A   S   S>

       340         350         360         370
  *    *    *    *    *    *    *    *    *    *
GCT GCT TCC AGT GCT GCT TCT TCA GTC ACT ACA ACT TTG ACG TCT
 A   A   S   S   A   A   S   S   V   T   T   T   L   T   S>

380         390         400         410         420
  *    *    *    *    *    *    *    *    *    *
TAT GGA CCA GCT GTA TTT TAC GCA CCT TCT GCA TCA TCT GGA GGC
 Y   G   P   A   V   F   Y   A   P   S   A   S   S   G   G>

       430         440         450         460
  *    *    *    *    *    *    *    *    *    *
TAT GGA GCT GGA GCT GGA GCT GTT GCT GCA GCA GGA GCT GCC GGC
 Y   G   A   G   A   G   A   V   A   A   A   G   A   A   G>

470         480         490         500         510
  *    *    *    *    *    *    *    *    *    *
GCT GGA GGT TAC GGA AGA GGT GCT GGA GGC TAC GGT GGA CAA GGA
 A   G   G   Y   G   R   G   A   G   G   Y   G   G   Q   G>
```

FIG. 1A

```
  520           530           540           550
   *     *       *     *       *     *       *     *       *
GGA TAT GGT GCC GGA GCC GGA GCT GGT GCT GCT GCA GCT GCT GGA
 G   Y   G   A   G   A   G   A   G   A   A   A   A   A   G>

560           570           580           590           600
  *     *       *     *       *     *       *     *       *
GCA GGA GCC GGA GGC GCT GGT GGT TAC GGT AGA GGT GCT GGT GCT
 A   G   A   G   G   A   G   G   Y   G   R   G   A   G   A>

        610           620           630           640
  *     *       *     *       *     *       *     *       *
GGA GCT GGT GCG GCT GCT GGG GCA GGT GCA GGC GCC GGT GGT GCT
 G   A   G   A   A   A   G   A   G   A   G   A   G   G   A>

650           660           670           680           690
  *     *       *     *       *     *       *     *       *
GGA TAT GGT GGA CAA GGC GGA TAT GGT GCC GGA GCA GGA GCT GGT
 G   Y   G   G   Q   G   G   Y   G   A   G   A   G   A   G>

        700           710           720           730
  *     *       *     *       *     *       *     *       *
GCG GCT GCT GCT GCT GGT GCA GGA GCA GGA GGT GCT GGC GGT TAC
 A   A   A   A   A   G   A   G   A   G   G   A   G   G   Y>

740           750           760           770           780
  *     *       *     *       *     *       *     *       *
GGT AGA GGT GCT GGT GCT GGA GCA GGA GCC GCT GCG GGT GCT GGA
 G   R   G   A   G   A   G   A   G   A   A   A   G   A   G>

        790           800           810           820
  *     *       *     *       *     *       *     *       *
GCT GGA GGC TAC GGT GGT CAA GGT GGG TAC GGT GCC GGA GCA GGA
 A   G   G   Y   G   G   Q   G   G   Y   G   A   G   A   G>

830           840           850           860           870
  *     *       *     *       *     *       *     *       *
GCT GGT GCG GCT GCT GCT GCT GCT GGA GCA GGA TCT GGA GGC GCT
 A   G   A   A   A   A   A   A   G   A   G   S   G   G   A>

        880           890           900           910
  *     *       *     *       *     *       *     *       *
GGC GGT TAC GGT AGA GGT GCT GGT GCT GGA GCT GGA GCC GCT GCA
 G   G   Y   G   R   G   A   G   A   G   A   G   A   A   A>

920           930           940           950           960
  *     *       *     *       *     *       *     *       *
GGT GCA GGA GCA GGA GCT GGA AGC TAC GGT GGT CAA GGA TAC GGT
 G   A   G   A   G   A   G   S   Y   G   G   Q   G   Y   G>

        970           980           990          1000
  *     *       *     *       *     *       *     *       *
GCC GGA GCA GGA GCT GGT GCT GCT GCA GCT GCA NNN NNN NNN NNN
 A   G   A   G   A   G   A   A   A   A   A
```

FIG. 1B

```
1010          1020          1030          1040
   *       *     *     *     *     *     *     *
NNN NNN NNN NNN NNN NNN NNN NNN NNN NNN GGT GCA GGT GCA
                                         G   A   G   A>

1050          1060          1070          1080          1090
   *     *       *     *     *     *     *     *     *
GGT GCT GGA TAT GGT GGA CAA GGC GGA TAT GGT GCC GGA GCA GGA
 G   A   G   Y   G   G   Q   G   G   Y   G   A   G   A   G>

      1100          1110          1120          1130
   *     *       *     *     *     *     *     *     *
GCT GGT GCG GCT GCT GCT GCT GGT GCA GGA GCT GGA GGT GCT GGT
 A   G   A   A   A   A   A   G   A   G   A   G   G   A   G>

1140          1150          1160          1170          1180
   *     *       *     *     *     *     *     *     *
GGT TAC GGT AGA GGT GCT GGT GCT GGA GCT GGA GCC GCT GCA GGT
 G   Y   G   R   G   A   G   A   G   A   G   A   A   A   G>

      1190          1200          1210          1220
   *     *       *     *     *     *     *     *     *
GCA GGA GCA GGA GCT GGA GGC TAC GGT GGT CAA AGT GGA TAC GGT
 A   G   A   G   A   G   G   Y   G   G   Q   S   G   Y   G>

1230          1240          1250          1260          1270
   *     *       *     *     *     *     *     *     *
GCC GGA GCA GGA GCT GCT GCA GCT GCT GGA GCA GGA GCT GGA GGC
 A   G   A   G   A   A   A   A   A   G   A   G   A   G   G>

      1280          1290          1300          1310
   *     *       *     *     *     *     *     *     *
GCT GGT GGT TAC GGT GA GGT GCT GGT GCT GGA GCA GGA GCC GCT
 A   G   G   Y   G   R   G   A   G   A   G   A   G   A   A>

1320          1330          1340          1350          1360
   *     *       *     *     *     *     *     *     *
GCG GGT GCT GGA GCA GGA GCC GCT GCG GGT GCA GGA GCT GGA GGC
 A   G   A   G   A   G   A   A   A   G   A   G   A   G   G>

      1370          1380          1390          1400
   *     *       *     *     *     *     *     *     *
TAC GGT GGT CAA GGT GGG TAC GGT GCC GGT GCA GGA GCT GGT GCG
 Y   G   G   Q   G   G   Y   G   A   G   A   G   A   G   A>

1410          1420          1430          1440          1450
   *     *       *     *     *     *     *     *     *
GCT GCT GCT GCT GGA GCA GGA GCT GGA GGC GCT GGT GGT TAC GGT
 A   A   A   A   G   A   G   A   G   G   A   G   G   Y   G>

      1460          1470          1480          1490
   *     *       *     *     *     *     *     *     *
AGA GGT GCT GGT GCT GGA GCT GGA GCT GCT GCA GGC GCA GGA GCT
 R   G   A   G   A   G   A   G   A   A   A   G   A   G   A>
```

FIG. 1C

```
1500          1510          1520          1530          1540
   *     *       *     *     *     *       *     *       *
   GGA GGC TAC GGT GGT CAA GGT GGA TAC GGT GCC GGA GCA GGA GCT
    G   G   Y   G   G   Q   G   G   Y   G   A   G   A   G   A>

      1550          1560          1570          1580
   *     *       *     *     *     *       *     *       *
   GGT GCT GCT GCA GCT GCT GCA ACA GGA GCC GGA GGC GCT GGT GGT
    G   A   A   A   A   A   A   T   G   A   G   G   A   G   G>

1590          1600          1610          1620          1630
   *     *       *     *     *     *       *     *       *
   TAC GGT AGA GGT GCT GGT GCT GGA GCT GGT GCC GCT GCT GGG GCA
    Y   G   R   G   A   G   A   G   A   G   A   A   A   G   A>

      1640          1650          1660          1670
   *     *       *     *     *     *       *     *       *
   GGT GCA GGC ACC GGT GGT GCT GGA TAT GGT GGA CAA GGC GGT TAT
    G   A   G   T   G   G   A   G   Y   G   G   Q   G   G   Y>

1680          1690          1700          1710          1720
   *     *       *     *     *     *       *     *       *
   GGT GCC GGA GCA GGA GCT GGT GCG GCT GCT GCT GCT GGT GCA GGA
    G   A   G   A   G   A   G   A   A   A   A   A   G   A   G>

      1730          1740          1750          1760
   *     *       *     *     *     *       *     *       *
   GCA GGA GGT GCT GGT TAC GGT AGA GGT GCT GGT GCT GGA GCT GGA
    A   G   G   A   G   Y   G   R   G   A   G   A   G   A   G>

1770          1780          1790          1800          1810
   *     *       *     *     *     *       *     *       *
   GCT GCT GCA GGT GCT GGA GCT GGA GCC GCT GCA GGT GCA GGA GCA
    A   A   A   G   A   G   A   G   A   A   A   G   A   G   A>

      1820          1830          1840          1850
   *     *       *     *     *     *       *     *       *
   GGA GCT GGA GGC TAC GGT GGT CAG GGT GGA TAC GGT GCC GGA GCA
    G   A   G   G   Y   G   G   Q   G   G   Y   G   A   G   A>

1860          1870          1880          1890          1900

   *     *       *     *     *     *       *     *       *
   AGA GCT GGT GCT GCG GCA GCT GCT GGA GCA GGA GCT GGA GGC GCT
    R   A   G   A   A   A   A   A   G   A   G   A   G   G   A>

      1910          1920          1930          1940
   *     *       *     *     *     *       *     *       *
   GCG GGT TAC AGT AGA GGT GGT CGT GCA GGA GCC GCT GGT GCT GGA
    A   G   Y   S   R   G   G   R   A   G   A   A   G   A   G>

1950          1960          1970          1980          1990
   *     *       *     *     *     *       *     *       *
   GCT GGA GCC GCT GCA GGT GCA GGA GCA GGA GCT GGA GGC TAC GGT
    A   G   A   A   A   G   A   G   A   G   A   G   G   Y   G>
```

FIG. 1D

```
   2000          2010          2020          2030
   *     *       *     *       *     *       *     *       *
   GGT CAA GGT GGA TAC GGT GCC GGA GCA GGA GCT GGT GCT GCT GCA
    G   Q   G   G   Y   G   A   G   A   G   A   G   A   A   A>

2040          2050          2060          2070          2080
   *     *       *     *       *     *       *     *       *
   GCT GCT GGT GCA GGA TCC GGA GGC GCT GGT GGT TAC GGT AGA GGT
    A   A   G   A   G   S   G   G   A   G   G   Y   G   R   G>

   2090          2100          2110          2120
   *     *       *     *       *     *       *     *       *
   GCT GGT GCT GGA GCC GCT GCA GGA GCT GGA GCC GCT GCA GGT GCT
    A   G   A   G   A   A   A   G   A   G   A   A   A   G   A>

2130          2140          2150          2160          2170
   *     *       *     *       *     *       *     *       *
   GGA GCA GGA GCT GGA GGC TAC GGT GGT CAA GGT GGA TAC GGT GCC
    G   A   G   A   G   G   Y   G   G   Q   G   G   Y   G   A>

   2180          2190          2200          2210
   *     *       *     *       *     *       *     *       *
   GGA GCA GGA GCT GCT GCA GCT GCT GGA GCA GGA GCC GGA CGT GGA
    G   A   G   A   A   A   A   A   G   A   G   A   G   R   G>

2220          2230          2240          2250          2260
   *     *       *     *       *     *       *     *       *
   GGT TAC GGA AGA GGT GCT GGT GCT GGA GGC TAC GGT GGA CAA GGA
    G   Y   G   R   G   A   G   A   G   G   Y   G   G   Q   G>

   2270          2280          2290          2300
   *     *       *     *       *     *       *     *       *
   GGA TAT GGT GCC GGA GCT GGA GCC GGT GCT GCT GCA GCT GCT GGA
    G   Y   G   A   G   A   G   A   G   A   A   A   A   A   G>

2310          2320          2330          2340          2350
   *     *       *     *       *     *       *     *       *
   GCG GGA GCC GGA GGC TAT GGC GAC AAG GAG ATA GCC TGC TGG AGC
    A   G   A   G   G   Y   G   D   K   E   I   A   C   W   S>

   2360          2370          2380          2390
   *     *       *     *       *     *       *     *       *
   AGG TGT AGA TAC ACT GTT GCC TCC ACA ACA TCT CGT TTG AGT TCG
    R   C   R   Y   T   V   A   S   T   T   S   R   L   S   S>

2400          2410          2420          2430          2440
   *     *       *     *       *     *       *     *       *
   GCC GAA GCA TCT TCT AGG ATA TCG TCG GCG GCT TCC ACT TTA GTA
    A   E   A   S   S   R   I   S   S   A   A   S   T   L   V>

   2450          2460          2470          2480
   *     *       *     *       *     *       *     *       *
   TCT GGA GGT TAC TTG AAT ACA GCA GCT CTG CCA TCG GTT ATT TCG
    S   G   G   Y   L   N   T   A   A   L   P   S   V   I   S>
```

FIG. 1E

```
2490          2500          2510          2520          2530
   *     *       *     *     *     *       *     *       *
   GAT CTT TTT GCC CAA GTT GGT GCA TCT TCT CCG GTG ATC AGA CAG
    D   L   F   A   Q   V   G   A   S   S   P   V   I   R   Q>

      2540          2550          2560          2570
   *     *       *     *     *     *       *     *       *
   CGA AGT TTG ATC CAA GTT TTG TTG GAA ATT GTT TCT TCT CTT ATC
    R   S   L   I   Q   V   L   L   E   I   V   S   S   L   I>

2580          2590          2600          2610          2620
   *     *       *     *     *     *       *     *       *
   CAT ATT CTC AGT TCT TCT AGC GTA GGA CAA GTC GAT TTC AGT TCG
    H   I   L   S   S   S   S   V   G   Q   V   D   F   S   S>

      2630          2640          2650          2660
   *     *       *     *     *     *       *     *       *
   GTT GGG TCG TCT GCT GCA GCT GTT GGT CAA TCC ATG CAA GTT GTA
    V   G   S   S   A   A   A   V   G   Q   S   M   Q   V   V>

2670          2680          2690          2700          2710
   *     *       *     *     *     *       *     *       *
   ATG GGC TAA ACAT GATGG TTCTC TCAAT TATGT ATTCT TTAAT TACCG
    M   G   *>

 2720          2730          2740          2750          2760
   *     *       *     *     *     *       *     *       *
   CTAAG GTAGC AAAAT ATTGT AAAGT AAAGT TTTCT TACAA AATAA AAATT

 2770          2780          2790
   *     *       *     *     *
   CTTTT CTGCA AAAAA AAAAA AAAAA AA
```

FIG. 1F

```
          10          20          30          40
     *    *    *    *    *    *    *    *    *
TCT TAT GGA CCA TCC GTA TTT TAC ACT CCT ACT TCA GCT GGA AGC
 S   Y   G   P   S   V   F   Y   T   P   T   S   A   G   S>

    50          60          70          80          90
     *    *    *    *    *    *    *    *    *    *
TAT GGT GCA GGG GCC GGA GGT TTT GGA GCT GGA GCC TCT GCT GGT
 Y   G   A   G   A   G   G   F   G   A   G   A   S   A   G>

          100         110         120         130
     *    *    *    *    *    *    *    *    *    *
GTC GGA GCC GGA GCT GGT ACT GTA GCA GGA TAT GGT GGA CAA GGA
 V   G   A   G   A   G   T   V   A   G   Y   G   G   Q   G>

   140         150         160         170         180
     *    *    *    *    *    *    *    *    *    *
GGA TAT GGT GCC GGA AGC GCT GGA GGT TAT GGA AGA GGT ACT GGA
 G   Y   G   A   G   S   A   G   G   Y   G   R   G   T   G>

          190         200         210         220
     *    *    *    *    *    *    *    *    *    *
GCT GGA GCC GCT GCT GGT GCC GGA GCA GGA GCC ACT GCT GGT GCC
 A   G   A   A   A   G   A   G   A   G   A   T   A   G   A>

   230         240         250         260         270
     *    *    *    *    *    *    *    *    *    *
GGA GCA GGA GCC GCT GCT GGT GCC GGA GCA GGA GCA GGT AAT TCA
 G   A   G   A   A   A   G   A   G   A   G   A   G   N   S>

          280         290         300
     *    *    *    *    *    *    *
GGA GGA TAT AGT GCC GGA GTA GGA GTT GGT GCT GCA GCT
 G   G   Y   S   A   G   V   G   V   G   A   A   A>
```

FIG. 2A

```
          10          20          30          40
     *    *    *     *    *     *    *     *
CT GCA GCT GCT GGA GGA GGT GCC GGA ACT GTT GGA GGT TAC GGA
    A   A   A   G   G   G   A   G   T   V   G   G   Y'  G>

     50          60          70          80
*    *    *     *    *     *    *     *    *
AGA GGT GCT GGT GTA GGA GCA GGT GCC GCT GCT GGT TTT GCG GCA
 R   G   A   G   V   G   A   G   A   A   A   G   F   A   A>

90        100         110         120         130
*    *    *     *    *     *    *     *    *
GGA GCT GGT GGT GCT GGA GGC TAC AGA AGA GAT GGA GGA TAC GGT
 G   A   G   G   A   G   G   Y   R   R   D   G   G   Y   G>

     140         150         160
*    *    *     *    *     *    *
GCT GGA GCA GGA GCT GGA GCT GCT GCA GCT G
 A   G   A   G   A   G   A   A   A   A   X>
```

FIG. 2B

```
          10          20          30          40
     *    *    *    *    *    *    *    *    *
GGT GCA GGA GGC TAT GGA AGA GGT GCT GGA GCT GGA GCT GCT GCA
 G   A   G   G   Y   G   R   G   A   G   A   G   A   A>

     50          60          70          80          90
     *    *    *    *    *    *    *    *    *
GTC GCA GGT GCA GAT GCT GGT GGC TAT GGA AGA AAT TAT GGT GCT
 V   A   G   A   D   A   G   G   Y   G   R   N   Y   G   A>

          100         110         120         130
     *    *    *    *    *    *    *    *    *
GGA ACC ACT GCT TAT GCA GGA GCC AGA GCC GGT GGT GCT GGA GGC
 G   T   T   A   Y   A   G   A   R   A   G   G   A   G   G>

    140         150         160         170         180
     *    *    *    *    *    *    *    *    *
TAT GGC GGA CAA GGA GGA TAT TCT TCT GGA GCC GGT GCT GCT GCA
 Y   G   G   Q   G   G   Y   S   S   G   A   G   A   A   A>

          190         200         210         220
     *    *    *    *    *    *    *    *    *
GCT TCT GGA GCA GGA GCC GAT ATC ACT AGT GGA TAC GGA AGA GGT
 A   S   G   A   G   A   D   I   T   S   G   Y   G   R   G>

    230         240         250         260         270
     *    *    *    *    *    *    *    *    *
GTT GGT GCT GGA GCT GGA GCA GAA ACT ATA GGT GCT GGA GGC TAT
 V   G   A   G   A   G   A   E   T   I   G   A   G   G   Y>

          280         290         300         310
     *    *    *    *    *    *    *    *    *
GGA GGT GGG GCT GGA TCA GGA GCA CGT GCG GCT TCA GCA TCC GGA
 G   G   G   A   G   S   G   A   R   A   A   S   A   S   G>

    320         330         340         350         360
     *    *    *    *    *    *    *    *    *
GCT GGT ACT GGA TAT GGT TCG TCT GGA GGT TAT AAC GTA GGT ACC
 A   G   T   G   Y   G   S   S   G   G   Y   N   V   G   T>

          370         380         390         400
     *    *    *    *    *    *    *    *    *
GGA ATA AGT ACT TCT TCT GGC GCT GCA TCT AGC TAC TCT GTT TCT
 G   I   S   T   S   S   G   A   A   S   S   Y   S   V   S>

    410         420         430         440         450
     *    *    *    *    *    *    *    *    *
GCT GGA GGT TAT GCT TCA ACA GGT GTT GGT ATT GGA TCC ACT GTT
 A   G   G   Y   A   S   T   G   V   G   I   G   S   T   V>

          460         470         480         490
     *    *    *    *    *    *    *    *    *
ACA TCC ACA ACA TCT CGT TTG AGT TCT GCT GAA GCA TGT TCT AGA
 T   S   T   T   S   R   L   S   S   A   E   A   C   S   R>
```

FIG. 2C

```
   500          510          520          530          540
    *    *    *    *    *    *    *    *    *    *    *
ATA TCT GCT GCG GCT TCC ACT TTA GTA TCT GGA TCC TTG AAT ACT
 I   S   A   A   A   S   T   L   V   S   G   S   L   N   T>

         550          560          570          580
    *    *    *    *    *    *    *    *    *    *    *
GCA GCT TTA CCA TCT GTA ATT TCG GAT CTT TTT GCC CAA GTT AGT
 A   A   L   P   S   V   I   S   D   L   F   A   Q   V   S>

   590          600          610          620          630
    *    *    *    *    *    *    *    *    *    *    *
GCA TCA TCA CCC GGG GTA TCA GGT AAC GAA GTT TTG ATT CAA GTT
 A   S   S   P   G   V   S   G   N   E   V   L   I   Q   V>

         640          650          660          670
    *    *    *    *    *    *    *    *    *    *    *
TTG TTG GAA ATT GTT TCT TCT CTT ATC CAT ATT CTT AGT TCT TCT
 L   L   E   I   V   S   S   L   I   H   I   L   S   S   S>

   680          690          700          710          720
    *    *    *    *    *    *    *    *    *    *    *
AGT GTA GGG CAA GTA GAT TTC AGT TCT GTT GGT TCA TCT GCT GCA
 S   V   G   Q   V   D   F   S   S   V   G   S   S   A   A>

         730          740          750          760
    *    *    *    *    *    *    *    *    *    *    *
GCC GTT GGT CAA TCC ATG CAA GTT GTA ATG GGT TAA AACA AAATG
 A   V   G   Q   S   M   Q   V   V   M   G   *>

  770          780          790          800          810
    *    *    *    *    *    *    *    *    *    *    *
GCTCT CTCTC TGTTA TATGC ATTCT GTAAT TTCTT CTAAA CTATT AAAAT

  820          830          840          850          860
    *    *    *    *    *    *    *    *    *    *    *
AATGT AATAA TTTCC TGCAT AAATA AAAAT ATTTT TCTGC AAAAA AAAAA

  870
    *
AAAAA
```

FIG. 2D

```
          10          20          30          40
     *    *    *     *    *     *    *     *    *
GCT GGA GCT GCT GCT GGT GCT GGA GGC TAT GAC GGA CAA GGA GGA TAT
 A   G   A   A   A   G   A   G   G   Y   D   G   Q   G   G   Y>

50          60          70          80          90
 *     *    *     *     *     *     *     *     *     *
GGT GCT GGA GCA GGA GCT GCT GCA GCT GCT GGA GCA GGA GCC GGA AGC
 G   A   G   A   G   A   A   A   A   A   G   A   G   A   G   S>

  100         110         120         130         140
    *     *     *     *     *     *     *     *     *
GTT GGA GGT TAT GGA ACA GGT GCT GTA GCT GGA TCT GGA ACA GCT GCT
 V   G   G   Y   G   T   G   A   V   A   G   S   G   T   A   A>

    150         160
*    *     *     *     *
GGT GCA GGA GCC AGA GCT GGT
 G   A   G   A   R   A   G>
```

FIG. 3A

```
          10          20          30          40
     *    *    *     *    *     *    *     *    *
GGA GCT GCT GCT GGT GCA GGA GCC GGA GCA GGT AGT ACA GGA GGC TTT
 G   A   A   A   G   A   G   A   G   A   G   S   T   G   G   F>

50          60          70          80          90
 *    *     *    *     *    *     *    *     *    *     *
GGC GGA CAA GGA GGA TAT GGT GCC GGT GCA GGA GCT GCA GCT GCT GGA
 G   G   Q   G   G   Y   G   A   G   A   G   A   A   A   A   G>

  100         110         120         130         140
    *    *     *    *     *    *     *    *     *    *
GCT TTT GCC GGA AGA GCT GGG GGT TAC GGA AGA GCT GCT GGA GCT GCG
 A   F   A   G   R   A   G   G   Y   G   R   A   A   G   A   A>

    150         160         170         180         190
*    *    *     *    *     *    *     *    *     *    *
GCT GGA ACT GGA GCT GCT GCT GGT GCA GGA GCC GGA GCT GGT AGT ACA
 A   G   T   G   A   A   A   G   A   G   A   G   A   G   S   T>

       200         210         220         230         240
  *    *    *     *    *     *    *     *    *     *    *
GGA GGC TTT GGC GGA CAA AGA GGA TAC GGT GCC GGC AGA AGT AAT GGA
 G   G   F   G   G   Q   R   G   Y   G   A   G   R   S   N   G>
```

FIG. 3B

```
          10        20        30        40
      *    *    *    *    *    *    *    *    *
TAT GGT GGA CAA GGC GGA TAT GGT GCT GGA GCA GGA GCT GGT GCT GCT
 Y   G   G   Q   G   G   Y   G   A   G   A   G   A   G   A   A>

50        60        70        80        90
 *    *    *    *    *    *    *    *    *    *
GCA GCC GCA GGA TAT GGA GCC GGT GCT GGA GGA TAC GGT GGA CAA GCT
 A   A   A   G   Y   G   A   G   A   G   G   Y   G   G   Q   A>

          100       110       120       130       140
      *    *    *    *    *    *    *    *    *    *
GGT TAT GGT GCC GGA GCT GGA GCT GGT AGT TCT GCA GGA AAT GCT TTC
 G   Y   G   A   G   A   G   A   G   S   S   A   G   N   A   F>
```

FIG. 3C

N-TERMINI: MiSP1 vs. MiSP2

```
MiSP1   M N N L L F A V S G Y V S T L G N A I S D A S A Y A N A L S S A I G N V L A N S G S I S E S T A S S A A S S
MiSP2

MiSP1   A A S S V T T T L T S Y G P A V F Y A P S A S S G G Y G A G A G A V A A A G A A G A G G Y G R G A G G Y G G
MiSP2             ...S Y G P S V F Y T P - T S A G S Y G A G A G A F G A G A S A G V G A G A G T V A G Y G G

MiSP1   Q G G Y G A G A G A G A A A A A G A G A G G A G G Y G R G A G A G A G A A A G A G A G A G G A ...
MiSP2   Q G   G Y G A G A G S A G G Y G R G T G A G A A A G A G A G A T A G A G A G A A A A G A G A G A G ...
```

C-TERMINI: MiSP1 vs. MiSP2

```
MiSP1   D K E I A C W S R C R Y T V A S T T S R L S S A E A S S R I S S A A S T L V S G G Y L N T A A L P S V I S D
MiSP2   G G Y A S T G V G I G S T V T S T T S R L S S A E A C S R I S A A A S T L V S G G S L N T A A L P S V I S D

MiSP1   L F A Q V G A S S P - V I R Q R S L I Q V L L E I V S S L I H I L S S S S V G W V D F S S V G S S A A A V G
MiSP2   L F A Q V S A S S P G V S G N E V L I Q V L L E I V S S L I H I L S S S S V G Q V D F S S V G S S A A A V G

MiSP1   Q S M Q V V M G Stop
MiSP2   Q S M Q V V M G Stop
```

FIG. 4

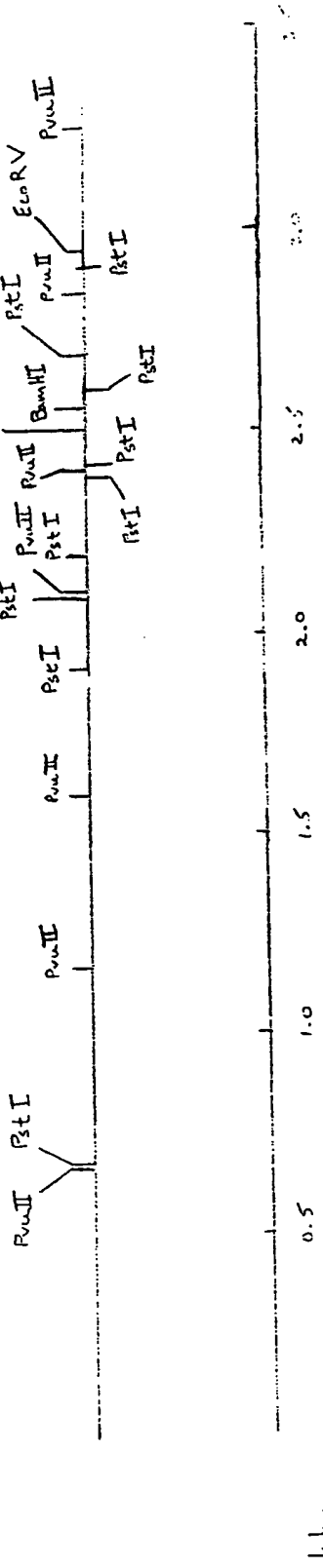
PvuII
PstI
PstI
PvuII
PvuII
PstI
PstI
PvuII
BamHI
PstI
PvuII
EcoRV
PvuII
PstI
PstI
PvuII
PvuII
0.5
1.0
1.5
2.0
2.5
kbp

Fig. 5

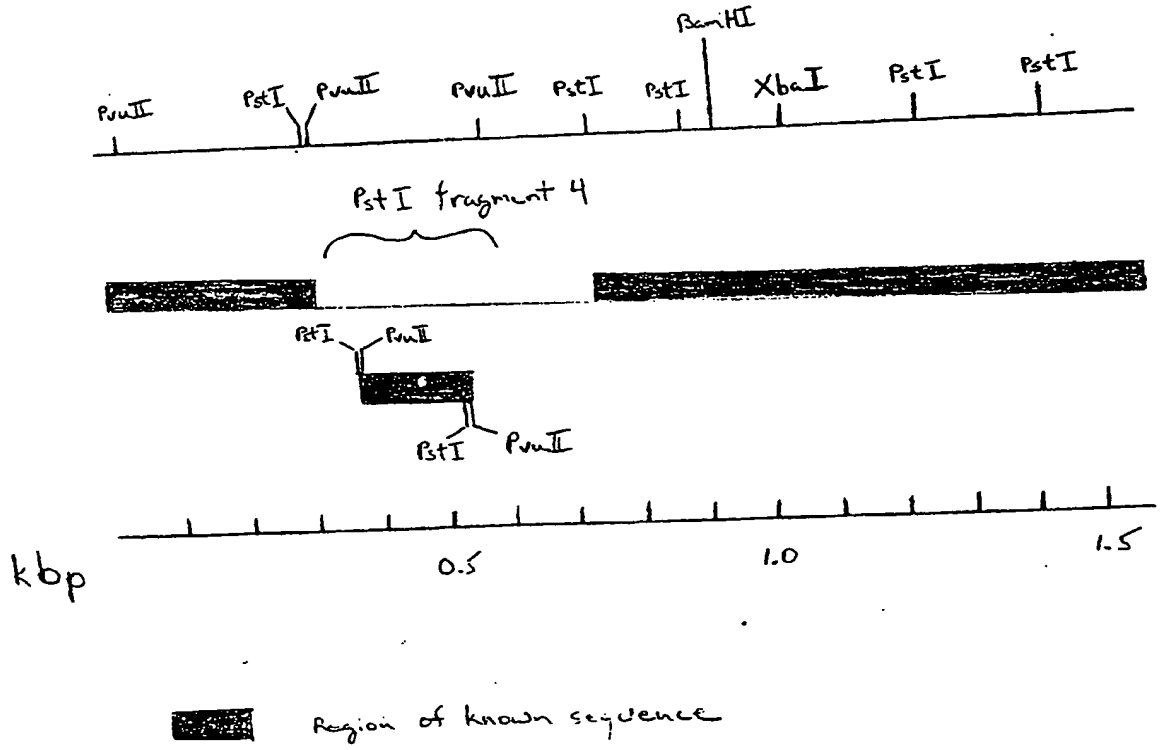
BamHI
PvuII
PstI
PvuII
PvuII
PstI
PstI
XbaI
PstI
PstI
PstI fragment 4
PstI
PvuII
PstI
PvuII
kbp
0.5
1.0
1.5
Region of known sequence

Fig. 6

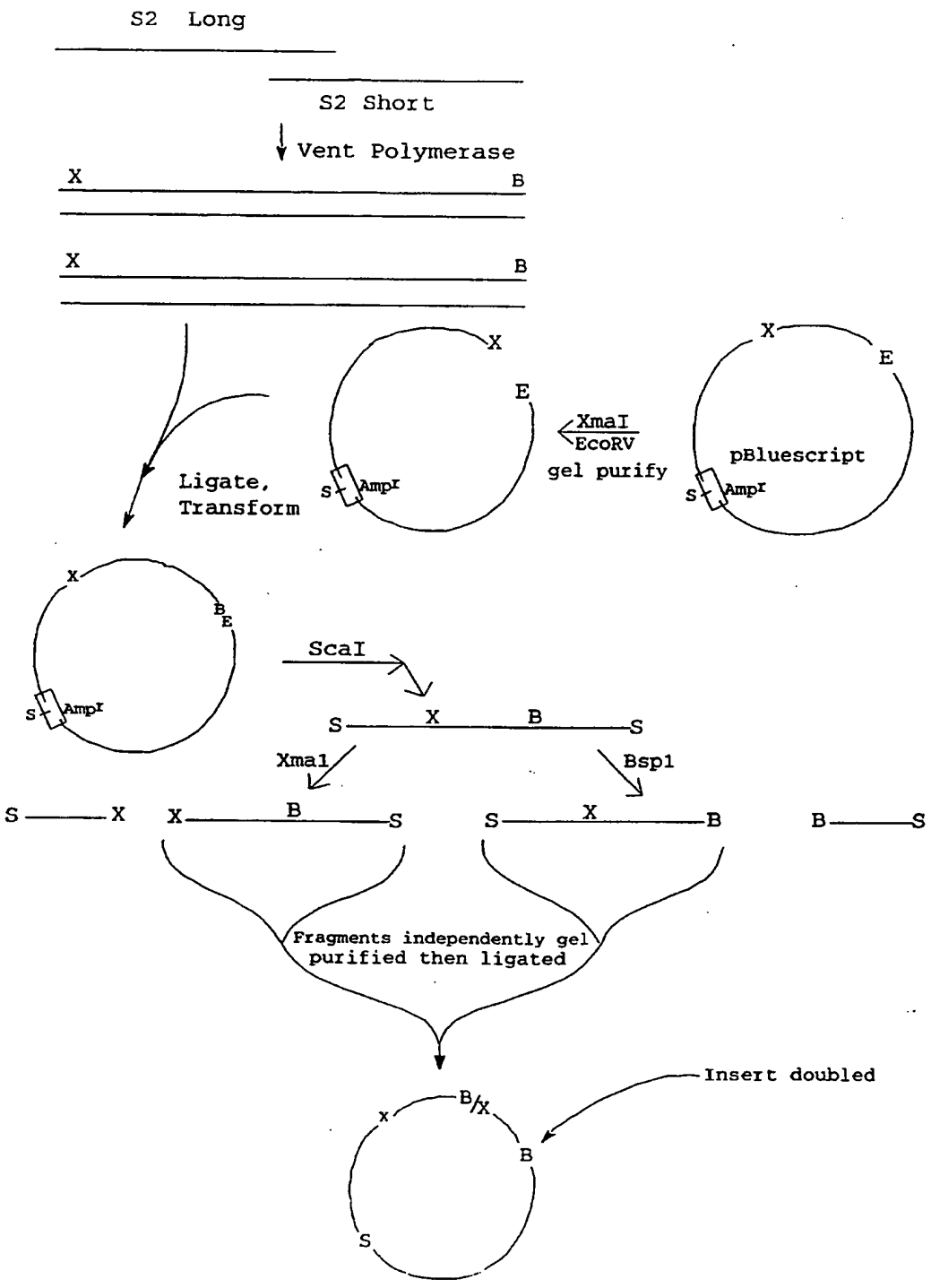
S2 Long
S2 Short
Vent Polymerase
X
B
Ligate,
Transform
XmaI
EcoRV
gel purify
pBluescript
Ampr
E
ScaI
S
Xmal
Bspl
Fragments independently gel purified then ligated
Insert doubled

Fig. 7

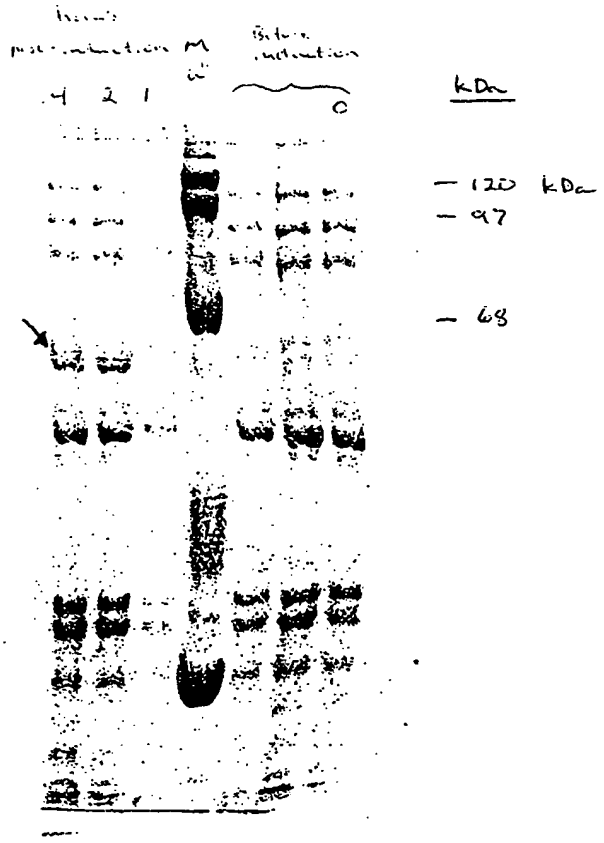

Fig. 8A

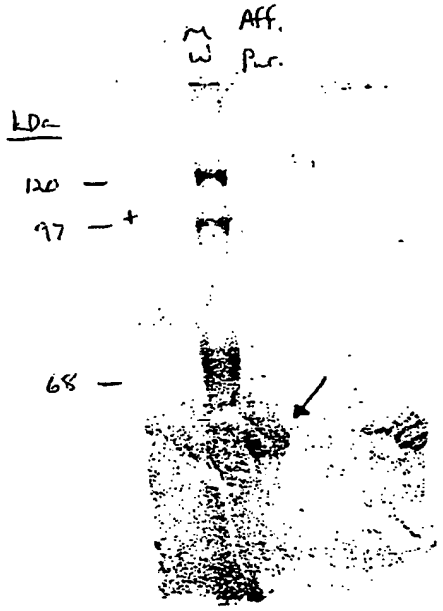

Fig. 8B

INTERNATIONAL SEARCH REPORT

Interna ıl Application No
PCT/US 95/03139

A. CLASSIFICATION OF SUBJECT MATTER
IPC 6 C12N15/12 C07K14/435 C12N1/19 C12N1/21 D01F4/00

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 6 C12N C07K D01F

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	EP,A,0 452 925 (THE UNIVERSITY OF WYOMING) 23 October 1991	21-23
A	see page 3, line 20 - line 31 see page 3, line 58 - page 4, line 25; table 1 see page 7, line 15 - line 27 see page 10, line 54 - page 11, line 4 see page 11, line 28 - page 12, line 8; examples 3-8	1-20,24

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"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
14 July 1995	07.08.95

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+ 31-70) 340-2040, Tx. 31 651 epo nl, Fax (+ 31-70) 340-3016	Montero Lopez, B

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X	PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, vol. 87, no. 18, September 1990 WASHINGTON US, pages 7120-7124, MING XU ET AL. 'Structure of a protein superfiber: Spider dragline silk'	21-23
A	see abstract see page 7121, right column, paragraph 3 - page 7123, left column, paragraph 3; figures 2,3	1-20,24
X	MATER. RES. SOC. SYMP. PROC. (1993), 292,(BIOMOLECULAR MATERIALS), 25-34 CODEN: MRSPDH;ISSN: 0272-9172, 1993 HINMAN, MIKE ET AL 'Spider silk proteins'	21-23
A	see page 30, paragraph 2 - page 33, paragraph 1; figures 1,2	1-20,24

3

INTERNATIONAL SEARCH REPORT

.formation on patent family members

Interr nal Application No
PCT/US 95/03139

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
EP-A-452925	23-10-91	JP-A- 6098771	12-04-94

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